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86

SEQ ID No. 4

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 5 LQDAIGSLHSRNVQVYGDVVLN HKAGADATEDVTAVEVNP
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 10 QSVFVDVPLHFNLQAASSQGGGYDMRRLLDGTVVSRHPEKA
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 VFYGD MYGTGKGTSPKEIPSLKDNIEPILKARKEYAYGPQH
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15

SEQ ID No. 5

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tgcctgaga

15

SEQ ID No. 6

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 20 LWLPPAYKGTSRSDVGYGVDLYDLGFEFNQKGTVRTKYGT
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 25 PSFFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYITKT
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SEQ ID No. 10

35 1 ATPADWRSQS IYFLLTDRFA RTDGSTTATC
 31 NTADQKYCGG TWQGIIDKLD YIQSMGFTAI
 61 WITPVTAQLP QTTAYGDAYH GYWQQDIYSL
 91 NENYGTADBL KALSSALHER GMYLMVDVVA

121 NHMGYDGAGS SVDYSVFKPF SSQDYFHPFC
151 FIQNYEDQTQ VEDCWLGDNT VSLPDLDTTK
181 DVVKNEWYDW VGSLVSNYSI DGLRIDTVKH
211 VQKDFWPGYN KAAGVYCIGE VLDGDPAYTC
5 241 PYQNVMDGVL NYPIYYPLLN AFKSTSGSMD
271 DLYNMINTVK SDCPDSTLLG TFVENHDNPR
301 FASYTNDIAL AKNVAAFIL NDGIPIIYAG
331 QEQHYAGGND PANREATWLS GYPTDSELYK
361 LIASANAIRN YAISKDTGFV TYKNWFIIYKD
10 391 DITIAMRKGT DGSQIVTILS NKGASGDSYT
421 LSLSGAGYTA GQQLTEVIGC TTVTVGSDGN
451 VPVPMAGGLP RVLYPTEKLA GSKICSSS

1	CB	VAL	A	1	11.9902	27.157	22.995	1.00	23.86	6	28.238	37.382	24.476	1.00	10.19	6
2	CG1	VAL	A	1	12.302	27.494	20.658	1.00	24.08	6	27.909	38.377	23.351	1.00	10.76	6
3	CE2	VAL	A	1	10.659	27.948	22.511	1.00	26.37	6	27.180	37.983	22.222	1.00	11.00	6
4	C	VAL	A	1	13.030	25.096	22.743	1.00	19.54	6	26.891	38.842	21.190	1.00	11.22	6
5	O	VAL	A	1	13.191	25.013	23.967	1.00	19.86	6	28.340	39.698	23.424	1.00	10.96	6
6	H	VAL	A	1	10.702	25.241	23.431	1.00	20.28	7	28.080	40.620	22.423	1.00	11.25	6
7	CA	VAL	A	1	11.659	25.658	23.335	1.00	20.25	6	27.358	40.156	21.312	1.00	11.62	6
8	H	ASH	A	2	13.867	24.729	21.802	1.00	18.39	7	27.114	41.063	20.294	1.00	11.87	8
9	CA	ASH	A	2	15.148	24.197	22.212	1.00	16.73	6	30.789	37.289	24.119	1.00	9.70	6
10	CB	ASH	A	2	15.836	23.657	20.945	1.00	16.09	6	30.918	38.427	24.563	1.00	9.67	8
11	CG	ASH	A	2	15.210	22.336	20.451	1.00	15.33	6	31.890	36.710	23.659	1.00	9.16	7
12	CG1	ASH	A	2	14.707	21.549	21.252	1.00	15.28	8	33.191	37.307	23.588	1.00	9.15	6
13	H02	ASH	A	2	15.263	22.082	19.751	1.00	12.41	7	33.805	37.750	24.961	1.00	8.08	6
14	C	ASH	A	2	15.949	25.134	22.767	1.00	15.71	6	33.968	36.659	25.978	1.00	9.21	6
15	O	ASH	A	2	15.803	26.435	22.108	1.00	16.82	8	35.239	36.135	26.240	1.00	10.15	6
16	H	GLY	A	3	16.720	25.198	23.853	1.00	14.56	7	32.887	36.171	26.720	1.00	7.79	6
17	CA	GLY	A	3	17.541	26.305	24.331	1.00	13.21	6	35.440	35.161	27.245	1.00	10.23	6
18	C	GLY	A	3	18.940	26.311	23.671	1.00	12.14	6	33.070	35.205	27.469	1.00	7.64	6
19	O	GLY	A	3	19.498	25.153	23.302	1.00	11.92	8	34.313	36.698	27.962	1.00	8.17	6
20	H	THR	A	4	19.503	27.368	23.999	1.00	11.28	7	33.903	35.102	22.910	1.00	8.65	8
21	CA	THR	A	4	20.829	27.555	22.912	1.00	10.96	6	34.173	36.294	22.963	1.00	8.94	6
22	CG1	THR	A	4	20.721	27.678	21.400	1.00	11.09	6	35.284	36.856	22.536	1.00	9.09	7
23	CG2	THR	A	4	19.930	26.828	20.782	1.00	12.31	8	36.430	36.089	22.006	1.00	9.38	6
24	C	THR	A	4	22.048	27.933	20.693	1.00	8.99	6	36.508	36.043	20.513	1.00	7.45	6
25	O	THR	A	4	21.584	28.664	23.683	1.00	10.56	6	36.684	37.345	19.740	1.00	7.55	6
26	H	LEU	A	5	21.080	29.743	23.866	1.00	9.98	6	37.901	37.580	19.356	1.00	8.81	6
27	CA	LEU	A	5	22.609	28.376	24.092	1.00	10.83	7	38.145	38.544	18.397	1.00	8.83	8
28	CG	LEU	A	5	23.700	28.277	25.789	1.00	9.31	6	38.962	36.877	19.438	1.00	5.00	8
29	CG1	LEU	A	5	24.515	28.446	26.864	1.00	10.96	6	37.590	37.807	22.737	1.00	9.92	8
30	CG2	LEU	A	5	25.429	28.946	26.864	1.00	9.46	6	37.590	37.807	22.737	1.00	10.15	7
31	CD1	LEU	A	5	24.887	30.150	27.608	1.00	9.46	6	38.793	36.059	22.729	1.00	10.35	6
32	CD2	LEU	A	5	25.608	27.882	27.894	1.00	10.35	6	39.988	36.551	23.607	1.00	9.98	6
33	C	LEU	A	5	24.644	29.992	25.840	1.00	10.65	6	41.182	35.619	23.186	1.00	9.98	6
34	O	LEU	A	5	25.047	29.453	22.798	1.00	10.85	6	42.273	35.940	24.181	1.00	11.61	6
35	H	MEI	A	6	25.071	31.217	28.132	1.00	10.94	6	42.292	35.583	25.525	1.00	12.44	6
36	CA	MEI	A	6	25.971	31.930	23.312	1.00	10.94	6	43.516	36.063	26.193	1.00	12.84	6
37	CG	MEI	A	6	25.453	33.143	22.507	1.00	12.97	6	41.412	34.916	26.432	1.00	11.39	6
38	CG1	MEI	A	6	26.629	33.643	21.838	1.00	15.17	6	43.446	36.606	23.915	1.00	11.78	6
39	CG2	MEI	A	6	27.525	35.144	19.516	1.00	16.94	6	46.188	36.673	23.083	1.00	12.99	7
40	CE	MEI	A	6	27.089	32.485	24.223	1.00	10.67	6	43.831	35.690	27.441	1.00	13.37	6
41	C	MEI	A	6	26.774	33.206	25.170	1.00	10.51	8	41.717	34.763	27.772	1.00	13.91	6
42	H	GLN	A	7	28.325	32.333	23.911	1.00	10.34	7	42.946	35.254	28.280	1.00	14.23	6
43	CA	GLN	A	7	29.440	32.727	24.681	1.00	10.20	6	40.410	37.937	22.933	1.00	10.57	6
44	CG	GLN	A	7	30.626	31.910	26.617	1.00	9.41	6	40.943	38.700	23.797	1.00	10.67	8
45	C	GLN	A	7	31.967	32.632	25.053	1.00	10.28	6	40.322	38.209	21.623	1.00	10.11	6
46	CG1	GLN	A	7	33.280	31.914	25.027	1.00	9.15	6	40.766	39.508	21.126	1.00	11.11	6
47	CG2	GLN	A	7	34.327	33.470	25.649	1.00	12.35	8	41.559	39.432	39.798	1.00	11.11	6
48	CE1	GLN	A	7	33.359	30.714	26.570	1.00	6.58	7	42.765	38.515	20.029	1.00	11.60	6
49	ME2	GLN	A	7	29.578	34.125	24.035	1.00	10.22	6	42.605	37.158	19.704	1.00	11.95	6
50	C	GLN	A	7	29.856	34.167	22.788	1.00	10.30	8	43.666	36.268	39.892	1.00	12.43	6
51	O	GLN	A	8	29.394	35.236	24.691	1.00	9.97	7	43.985	38.951	20.540	1.00	11.68	6
52	H	THR	A	8	29.667	36.526	24.022	1.00	9.95	6	45.023	38.076	20.714	1.00	11.85	6
53	CA	THR	A	8	29.447	36.526	24.022	1.00	9.95	6	44.878	38.749	20.368	1.00	12.61	6

ATOM	107	OK	YR	A	12	45.854	35.787	20.560	1.00	13.18	6	ATOM	160	HE2	HE1	A	19	31.584	41.112	24.073	1.00	9.42	7
ATOM	108	C	YR	A	12	39.687	40.574	20.991	1.00	11.38	6	ATOM	161	C	HE1	A	19	30.007	45.489	25.132	1.00	9.04	6
ATOM	109	O	YR	A	12	39.862	41.436	20.132	1.00	11.53	8	ATOM	162	O	HE1	A	19	29.153	44.638	24.493	1.00	8.75	8
ATOM	110	X	YR	A	13	38.630	40.547	21.783	1.00	11.49	7	ATOM	163	H	YR	A	20	29.650	46.184	26.217	1.00	9.17	7
ATOM	111	CA	YR	A	13	37.651	41.856	21.760	1.00	11.50	6	ATOM	164	CA	YR	A	20	28.268	46.090	26.688	1.00	9.56	6
ATOM	112	CA	YR	A	13	36.604	41.321	22.761	1.00	13.32	6	ATOM	165	CB	YR	A	20	28.200	46.691	28.093	1.00	8.24	6
ATOM	113	CG1	YR	A	13	35.755	40.298	22.169	1.00	14.85	8	ATOM	166	CG	YR	A	20	29.112	46.119	29.122	1.00	7.50	6
ATOM	114	CG2	YR	A	13	35.732	42.466	23.175	1.00	14.00	6	ATOM	167	CG2	YR	A	20	29.515	44.774	29.341	1.00	7.46	6
ATOM	115	C	YR	A	13	38.689	42.880	22.036	1.00	11.41	6	ATOM	168	CE2	YR	A	20	30.374	44.751	30.459	1.00	7.35	6
ATOM	116	O	YR	A	13	39.429	42.805	22.840	1.00	11.13	8	ATOM	169	CE3	YR	A	20	39.187	43.568	28.695	1.00	8.23	6
ATOM	117	H	YR	A	14	38.254	44.035	21.408	1.00	11.47	7	ATOM	170	CO1	YR	A	20	39.738	46.854	30.088	1.00	7.37	6
ATOM	118	CO	YR	A	14	37.104	44.144	20.397	1.00	11.68	6	ATOM	171	HE1	YR	A	20	30.483	46.041	30.920	1.00	7.58	7
ATOM	119	CA	YR	A	14	38.979	45.243	21.611	1.00	11.44	6	ATOM	172	CE2	YR	A	20	30.926	43.591	31.006	1.00	6.78	6
ATOM	120	CB	YR	A	14	38.477	46.296	20.589	1.00	11.68	6	ATOM	173	CE3	YR	A	20	29.750	42.407	29.223	1.00	9.26	6
ATOM	121	CO	YR	A	14	37.352	45.504	19.896	1.00	11.77	6	ATOM	174	CE2	YR	A	20	30.608	42.427	30.366	1.00	7.69	6
ATOM	122	C	YR	A	14	38.786	45.868	22.993	1.00	11.21	6	ATOM	175	C	YR	A	20	27.227	46.746	35.757	1.00	9.73	6
ATOM	123	O	YR	A	14	37.783	45.785	23.618	1.00	11.15	8	ATOM	176	O	YR	A	20	26.870	46.395	25.592	1.00	9.42	8
ATOM	124	H	YR	A	15	39.005	46.557	23.445	1.00	10.84	7	ATOM	177	H	YR	A	21	27.591	47.832	25.102	1.00	10.37	7
ATOM	125	CA	YR	A	15	39.720	47.304	24.693	1.00	11.02	6	ATOM	178	CA	YR	A	21	26.731	48.544	24.144	1.00	11.41	6
ATOM	126	CB	YR	A	15	41.073	47.318	25.411	1.00	11.27	6	ATOM	179	CB	YR	A	21	27.368	49.858	25.671	1.00	15.11	6
ATOM	127	CG	YR	A	15	41.055	48.267	26.414	1.00	11.89	6	ATOM	180	CG	YR	A	21	27.086	50.981	24.674	1.00	21.25	6
ATOM	128	CO1	YR	A	15	40.808	48.358	27.377	1.00	12.57	8	ATOM	181	CO	YR	A	21	28.020	52.128	24.411	1.00	23.92	6
ATOM	129	HE2	YR	A	15	42.158	48.898	26.922	1.00	11.38	7	ATOM	182	CE	YR	A	21	27.000	53.426	25.067	1.00	30.86	6
ATOM	130	C	YR	A	15	39.240	48.737	24.377	1.00	11.05	6	ATOM	183	HE	YR	A	21	27.119	54.648	24.030	1.00	36.43	7
ATOM	131	O	YR	A	15	39.932	49.767	24.524	1.00	11.08	8	ATOM	184	C	YR	A	21	26.551	47.632	22.934	1.00	11.59	6
ATOM	132	H	YR	A	16	38.008	48.835	23.905	1.00	10.98	7	ATOM	185	O	YR	A	21	25.474	47.562	22.400	1.00	11.80	8
ATOM	133	CA	YR	A	16	37.466	50.118	23.529	1.00	11.17	6	ATOM	186	H	YR	A	22	27.626	46.953	22.545	1.00	11.87	7
ATOM	134	CA	YR	A	16	36.954	50.059	22.868	1.00	11.59	6	ATOM	187	CA	YR	A	22	27.576	46.015	21.451	1.00	12.42	6
ATOM	135	CB	YR	A	16	35.761	49.101	21.873	1.00	12.89	6	ATOM	188	CB	YR	A	22	28.940	45.391	21.199	1.00	12.84	6
ATOM	136	CG1	YR	A	16	35.313	48.341	22.772	1.00	11.83	6	ATOM	189	CG	YR	A	22	29.804	46.215	20.240	1.00	13.26	6
ATOM	137	CG2	YR	A	16	35.264	49.114	20.732	1.00	14.31	8	ATOM	190	CG	YR	A	22	31.043	45.363	19.942	1.00	14.67	6
ATOM	138	C	YR	A	16	36.352	50.518	24.498	1.00	11.03	6	ATOM	191	HE	YR	A	22	32.084	45.253	20.955	1.00	14.04	7
ATOM	139	O	YR	A	16	35.768	51.582	24.889	1.00	11.12	8	ATOM	192	C2	YR	A	22	33.088	46.181	21.005	1.00	14.66	6
ATOM	140	H	YR	A	17	36.013	49.732	25.513	1.00	10.89	7	ATOM	193	HE1	YR	A	22	33.913	45.855	22.063	1.00	13.42	7
ATOM	141	CA	YR	A	17	34.972	50.083	26.479	1.00	10.61	6	ATOM	194	HE2	YR	A	22	33.206	47.242	20.261	1.00	12.34	7
ATOM	142	C	YR	A	17	33.545	50.032	25.938	1.00	10.65	6	ATOM	195	C	YR	A	22	25.588	44.921	21.812	1.00	13.77	6
ATOM	143	O	YR	A	17	32.679	50.522	26.881	1.00	10.67	8	ATOM	196	O	YR	A	22	25.682	44.543	21.038	1.00	13.11	8
ATOM	144	H	YR	A	18	35.287	49.436	24.746	1.00	10.50	7	ATOM	197	H	YR	A	23	26.678	44.342	23.082	1.00	12.84	7
ATOM	145	CA	YR	A	18	31.995	49.346	24.151	1.00	10.55	6	ATOM	198	CA	YR	A	23	25.698	43.292	23.370	1.00	12.86	6
ATOM	146	CB	YR	A	18	32.064	49.835	22.691	1.00	11.25	6	ATOM	199	CB	YR	A	23	26.092	42.716	24.721	1.00	10.88	6
ATOM	147	CG	YR	A	18	32.718	51.182	22.536	1.00	21.24	6	ATOM	200	CG	YR	A	23	25.124	41.739	25.381	1.00	10.16	6
ATOM	148	CO	YR	A	18	31.729	52.313	22.693	1.00	25.84	6	ATOM	201	CO1	YR	A	23	24.804	40.562	24.449	1.00	8.43	6
ATOM	149	HE1	YR	A	18	30.674	52.415	22.816	1.00	29.22	8	ATOM	202	CO2	YR	A	23	25.769	41.258	24.669	1.00	9.16	6
ATOM	150	HE2	YR	A	18	32.104	53.124	23.668	1.00	27.29	7	ATOM	203	C	YR	A	23	24.265	43.874	23.388	1.00	13.25	6
ATOM	151	C	YR	A	18	31.421	47.936	24.942	1.00	10.04	6	ATOM	204	O	YR	A	23	23.302	43.267	22.969	1.00	12.84	8
ATOM	152	O	YR	A	18	30.467	47.808	23.281	1.00	9.96	8	ATOM	205	H	YR	A	24	24.144	45.123	23.873	1.00	13.66	7
ATOM	153	H	YR	A	19	31.986	46.944	24.702	1.00	9.66	7	ATOM	206	CA	YR	A	24	22.848	45.781	23.929	1.00	14.44	6
ATOM	154	CA	YR	A	19	31.448	45.572	24.582	1.00	9.29	6	ATOM	207	CB	YR	A	24	22.959	47.205	24.523	1.00	16.39	6
ATOM	155	CB	YR	A	19	32.412	44.535	25.162	1.00	6.70	6	ATOM	208	CG	YR	A	24	21.578	47.851	24.620	1.00	18.17	6
ATOM	156	CG	YR	A	19	33.091	43.173	24.563	1.00	8.79	6	ATOM	209	CG	YR	A	24	21.659	49.208	25.596	1.00	20.10	6
ATOM	157	CO2	YR	A	19	31.749	41.967	23.188	1.00	7.93	6	ATOM	210	CE1	YR	A	24	22.851	49.936	25.205	1.00	21.30	8
ATOM	158	CO1	YR	A	19	32.114	42.955	23.187	1.00	8.36	7	ATOM	211	HE2	YR	A	24	22.819	49.539	26.823	1.00	28.53	7
ATOM	159	CE1	YR	A	19	31.805	41.705	22.909	1.00	8.32	6	ATOM	212	C	YR	A	24	22.208	45.914	22.528	1.00	14.70	6

213	ATOM	213	O	GLN A	24	21.030	45.626	22.296	1.00 14.63	8	ATOM	266	C	SER A	31	15.995	36.112	18.852	1.00 16.34	6	
214	ATOM	214	H	ASN A	25	23.034	46.369	21.594	1.00 14.90	7	ATOM	267	O	SER A	31	15.558	34.966	18.878	1.00 16.30	8	
215	ATOM	215	CA	ASN A	25	22.642	46.525	20.213	1.00 15.31	6	ATOM	268	H	ASP A	32	16.021	36.882	17.745	1.00 16.40	7	
216	ATOM	216	CA	ASN A	25	23.645	47.256	19.304	1.00 18.01	6	ATOM	269	CA	ASP A	32	15.477	36.341	16.518	1.00 16.55	6	
217	ATOM	217	CG	ASN A	25	23.711	48.719	19.880	1.00 22.28	6	ATOM	270	CG	ASP A	32	15.485	37.339	15.370	1.00 22.70	6	
218	ATOM	218	CG	ASN A	25	22.686	49.238	20.127	1.00 24.46	6	ATOM	271	CG	ASP A	32	14.756	38.665	15.583	1.00 27.13	6	
219	ATOM	219	CG	ASN A	25	24.036	49.632	19.568	1.00 23.11	7	ATOM	272	CG	ASP A	32	13.849	38.871	16.443	1.00 29.59	8	
220	ATOM	220	H	ASN A	25	22.371	45.141	19.588	1.00 15.19	6	ATOM	273	CG	ASP A	32	15.122	39.661	14.668	1.00 29.28	8	
221	ATOM	221	O	ASN A	25	21.542	45.198	18.637	1.00 15.31	8	ATOM	274	C	ASP A	32	16.207	35.103	14.032	1.00 16.39	6	
222	ATOM	222	H	ASP A	26	22.956	44.059	20.051	1.00 14.67	7	ATOM	275	O	ASP A	32	15.416	34.249	15.583	1.00 16.54	8	
223	ATOM	223	CA	ASP A	26	22.647	42.765	19.394	1.00 14.68	6	ATOM	276	H	ILE A	33	17.519	34.862	16.111	1.00 15.83	7	
224	ATOM	224	CG	ASP A	26	24.002	42.002	19.440	1.00 14.63	6	ATOM	277	CA	ILE A	33	18.093	33.612	15.639	1.00 15.16	6	
225	ATOM	225	CG	ASP A	26	24.340	41.059	18.322	1.00 14.74	6	ATOM	278	CG	ILE A	33	19.570	33.804	15.292	1.00 13.80	6	
226	ATOM	226	CG	ASP A	26	23.651	41.073	17.292	1.00 14.77	8	ATOM	279	CG	ILE A	33	19.681	34.906	14.219	1.00 11.75	6	
227	ATOM	227	CG	ASP A	26	25.294	40.238	18.363	1.00 14.65	8	ATOM	280	CG	ILE A	33	20.353	34.167	16.549	1.00 13.86	6	
228	ATOM	228	C	ASP A	26	21.497	41.933	19.949	1.00 14.18	6	ATOM	281	CG	ILE A	33	21.822	36.372	16.151	1.00 14.13	6	
229	ATOM	229	C	ASP A	26	21.119	40.869	19.454	1.00 13.76	8	ATOM	282	C	ILE A	33	17.939	32.408	16.568	1.00 15.00	6	
230	ATOM	230	H	ALA A	27	20.813	42.356	20.986	1.00 16.32	7	ATOM	283	O	ILE A	34	18.342	31.264	16.207	1.00 15.28	8	
231	ATOM	231	CA	ALA A	27	19.761	41.841	21.661	1.00 16.78	6	ATOM	284	H	GLY A	34	17.303	32.527	17.740	1.00 14.35	7	
232	ATOM	232	CG	ALA A	27	19.276	42.435	22.849	1.00 12.97	6	ATOM	285	CA	GLY A	34	17.113	31.380	18.606	1.00 13.52	6	
233	ATOM	233	C	ALA A	27	18.627	41.287	20.754	1.00 15.34	6	ATOM	286	C	GLY A	34	18.042	31.279	19.790	1.00 12.87	8	
234	ATOM	234	H	GLU A	28	18.231	40.028	20.840	1.00 15.78	7	ATOM	287	O	GLY A	34	18.034	30.216	20.453	1.00 12.97	8	
235	ATOM	235	H	GLU A	28	18.899	42.032	19.858	1.00 15.78	7	ATOM	288	H	ILE A	35	18.796	32.320	20.120	1.00 12.23	7	
236	ATOM	236	CA	GLU A	28	17.010	41.598	18.984	1.00 16.05	6	ATOM	289	CA	ILE A	35	19.879	32.268	21.301	1.00 11.16	6	
237	ATOM	237	CG	GLU A	28	16.526	42.815	18.170	1.00 23.00	6	ATOM	290	CG	ILE A	35	20.812	33.277	21.168	1.00 9.65	6	
238	ATOM	238	CG	GLU A	28	15.097	42.736	17.596	1.00 31.01	6	ATOM	291	CG	ILE A	35	21.595	33.376	22.527	1.00 8.10	6	
239	ATOM	239	CD	GLU A	28	14.001	42.258	18.547	1.00 38.48	6	ATOM	292	CG	ILE A	35	21.762	33.025	20.802	1.00 9.07	6	
240	ATOM	240	OE1	GLU A	28	13.644	41.013	18.587	1.00 40.16	6	ATOM	293	CD	ILE A	35	22.447	31.654	19.909	1.00 8.99	6	
241	ATOM	241	OE2	GLU A	28	13.427	43.089	19.318	1.00 38.33	8	ATOM	294	C	ILE A	35	18.798	32.522	22.516	1.00 10.71	6	
242	ATOM	242	C	GLU A	28	17.410	40.467	18.044	1.00 15.55	6	ATOM	295	C	ILE A	35	18.050	33.521	22.584	1.00 10.65	8	
243	ATOM	243	O	GLU A	28	16.773	39.435	17.835	1.00 15.27	8	ATOM	296	H	THR A	36	18.816	31.638	23.319	1.00 10.23	7	
244	ATOM	244	H	ILE A	29	18.577	40.712	17.415	1.00 15.36	7	ATOM	297	CA	THR A	36	17.144	30.682	24.713	1.00 7.65	6	
245	ATOM	245	CA	ILE A	29	19.158	39.769	16.661	1.00 15.11	6	ATOM	298	CG	THR A	36	18.091	29.405	25.089	1.00 7.88	8	
246	ATOM	246	CG	ILE A	29	20.592	40.422	16.688	1.00 16.22	6	ATOM	299	CG	THR A	36	16.198	30.293	23.779	1.00 6.33	6	
247	ATOM	247	CG	ILE A	29	21.296	39.400	15.259	1.00 18.29	6	ATOM	300	CG	THR A	36	18.844	32.120	25.955	1.00 9.79	6	
248	ATOM	248	CG	ILE A	29	20.895	38.501	14.294	1.00 18.16	6	ATOM	301	C	THR A	36	18.271	32.449	26.995	1.00 9.82	8	
249	ATOM	249	MO1	ILE A	29	22.839	39.155	15.496	1.00 18.52	7	ATOM	302	O	THR A	36	20.160	32.045	25.937	1.00 9.41	7	
250	ATOM	250	OE1	ILE A	29	21.055	38.163	14.693	1.00 18.61	6	ATOM	303	H	ALA A	37	20.978	32.392	27.086	1.00 9.45	6	
251	ATOM	251	ME2	ILE A	29	22.006	37.741	13.984	1.00 18.61	7	ATOM	304	CA	ALA A	37	21.169	31.279	28.113	1.00 9.60	6	
252	ATOM	252	C	ILE A	29	19.282	38.370	17.059	1.00 14.68	6	ATOM	305	CG	ALA A	37	22.309	32.897	26.536	1.00 9.43	6	
253	ATOM	253	O	ILE A	29	18.952	37.340	16.543	1.00 14.68	7	ATOM	306	C	ALA A	37	22.815	32.583	25.562	1.00 9.36	8	
254	ATOM	254	H	LEU A	30	19.913	38.292	18.233	1.00 14.64	7	ATOM	307	O	ALA A	37	22.871	33.921	27.171	1.00 9.63	7	
255	ATOM	255	CA	LEU A	30	20.154	37.107	19.020	1.00 14.56	6	ATOM	308	H	VAL A	38	24.164	36.496	26.853	1.00 9.68	6	
256	ATOM	256	CB	LEU A	30	20.913	37.409	20.319	1.00 13.60	6	ATOM	309	CA	VAL A	38	24.047	35.995	26.455	1.00 12.81	6	
257	ATOM	257	CG	LEU A	30	22.350	37.884	20.194	1.00 15.00	6	ATOM	310	CG	VAL A	38	25.397	36.673	26.790	1.00 14.06	6	
258	ATOM	258	CG	LEU A	30	23.018	37.967	21.586	1.00 15.90	6	ATOM	311	CG	VAL A	38	23.287	36.191	25.123	1.00 12.91	6	
259	ATOM	259	CG	LEU A	30	23.239	37.069	19.292	1.00 14.94	6	ATOM	312	CG	VAL A	38	25.134	34.526	28.042	1.00 9.49	6	
260	ATOM	260	C	LEU A	30	18.833	36.434	19.390	1.00 14.68	6	ATOM	313	C	VAL A	38	24.728	34.563	29.197	1.00 9.46	8	
261	ATOM	261	O	LEU A	30	18.683	35.228	19.248	1.00 14.21	8	ATOM	314	C	VAL A	38	26.371	33.915	27.799	1.00 9.08	7	
262	ATOM	262	H	SER A	31	17.817	37.240	19.879	1.00 15.37	7	ATOM	315	H	TRP A	39	28.188	32.692	28.797	1.00 7.03	6	
263	ATOM	263	CA	SER A	31	16.596	36.559	20.284	1.00 18.15	6	ATOM	316	CA	TRP A	39	29.612	32.554	29.282	1.00 6.23	6	
264	ATOM	264	CB	SER A	31	15.603	37.378	21.005	1.00 17.82	6	ATOM	317	CB	TRP A	39						
265	ATOM	265	CG	SER A	31	15.358	38.528	20.190	1.00 22.98	8	ATOM	318	CG	TRP A	39						

319	CD2	HP	A	39	30.691	31.682	20.807	1.00	6.00	6	ATOM	372	CD	LYS	A	45	39.093	48.024	37.024	1.00	5.00	6
320	CE2	HP	A	39	31.875	32.074	29.473	1.00	5.58	6	ATOM	373	CE	LYS	A	45	37.830	46.865	36.976	1.00	5.00	6
321	CE3	HP	A	39	30.708	30.585	27.908	1.00	5.74	6	ATOM	374	CE	LYS	A	45	37.599	49.990	37.908	1.00	5.00	7
322	CD1	HP	A	39	30.303	33.372	30.198	1.00	5.14	6	ATOM	375	C	LYS	A	45	39.029	44.010	37.657	1.00	5.87	6
323	HE1	HP	A	39	31.568	33.153	30.268	1.00	5.57	7	ATOM	376	O	LYS	A	45	39.207	43.306	30.636	1.00	5.70	8
324	CE2	HP	A	39	33.099	31.441	29.211	1.00	5.00	6	ATOM	377	H	GLY	A	46	39.847	43.978	36.608	1.00	6.09	7
325	CE3	HP	A	39	31.995	29.964	27.701	1.00	5.00	6	ATOM	378	CA	GLY	A	46	41.017	43.169	36.478	1.00	6.70	6
326	CD2	HP	A	39	33.115	30.400	28.307	1.00	5.00	6	ATOM	379	C	GLY	A	46	42.246	43.917	36.957	1.00	7.41	8
327	C	HP	A	39	28.317	35.078	28.452	1.00	8.53	6	ATOM	380	D	GLY	A	46	42.171	45.098	37.382	1.00	7.54	8
328	O	HP	A	39	28.036	35.399	27.384	1.00	8.32	8	ATOM	381	H	LEU	A	47	43.420	43.291	36.970	1.00	7.77	7
329	H	LE	A	40	28.431	35.945	29.459	1.00	8.37	7	ATOM	382	CA	LEU	A	47	44.681	43.889	37.305	1.00	8.34	6
330	CA	LE	A	40	29.143	37.247	29.467	1.00	8.51	6	ATOM	383	CB	LEU	A	47	45.638	42.922	37.455	1.00	9.18	6
331	CB	LE	A	40	29.091	38.113	30.259	1.00	9.85	6	ATOM	384	CE	LEU	A	47	46.426	42.160	36.297	1.00	11.32	6
332	CE2	LE	A	40	28.989	38.802	31.613	1.00	9.64	6	ATOM	385	CD1	LEU	A	47	45.419	41.207	35.660	1.00	12.40	6
333	CE3	LE	A	40	27.803	39.287	29.286	1.00	9.52	6	ATOM	386	CD2	LEU	A	47	46.897	42.995	35.137	1.00	12.34	6
334	CD1	LE	A	40	26.934	38.637	28.616	1.00	11.76	6	ATOM	387	C	LEU	A	47	45.040	45.105	36.483	1.00	8.70	6
335	C	LE	A	40	30.524	37.121	30.043	1.00	8.39	6	ATOM	388	D	LEU	A	47	45.884	45.929	36.872	1.00	8.67	8
336	O	LE	A	40	30.680	36.373	31.033	1.00	8.04	6	ATOM	389	H	SER	A	48	44.451	45.283	35.303	1.00	8.86	7
337	H	PR	A	41	31.571	37.800	29.566	1.00	8.30	7	ATOM	390	CA	SER	A	48	44.667	46.453	34.457	1.00	9.11	6
338	CB	PR	A	41	31.469	38.773	28.451	1.00	8.06	6	ATOM	391	CB	SER	A	48	45.870	46.312	33.492	1.00	9.17	6
339	CA	PR	A	41	32.887	37.771	30.151	1.00	8.14	6	ATOM	392	OC	SER	A	48	45.546	45.387	32.490	1.00	8.88	8
340	CB	PR	A	41	32.802	38.683	29.246	1.00	8.1	6	ATOM	393	C	SER	A	48	43.380	46.878	33.672	1.00	9.13	6
341	CO	PR	A	41	32.756	39.565	28.995	1.00	8.01	6	ATOM	394	O	SER	A	48	42.533	45.777	33.610	1.00	9.05	6
342	C	PR	A	41	32.846	38.312	31.590	1.00	7.87	6	ATOM	395	CA	GLN	A	49	43.225	47.807	33.003	1.00	9.23	7
343	O	PR	A	41	31.891	38.952	32.039	1.00	7.72	6	ATOM	396	CA	GLN	A	49	42.076	48.113	32.174	1.00	9.17	6
344	H	PR	A	42	33.939	38.046	32.341	1.00	7.64	7	ATOM	397	CB	GLN	A	49	42.104	49.549	31.592	1.00	6.81	6
345	CO	PR	A	42	35.113	37.297	31.880	1.00	7.36	6	ATOM	398	CG	GLN	A	49	40.813	49.921	30.864	1.00	5.86	6
346	CA	PR	A	42	34.084	38.542	31.711	1.00	7.41	6	ATOM	399	CD	GLN	A	49	41.078	51.178	30.043	1.00	7.48	6
347	CB	PR	A	42	35.400	38.085	34.191	1.00	7.45	6	ATOM	400	OE1	GLN	A	49	41.898	51.153	29.103	1.00	7.62	8
348	CG	PR	A	42	35.772	36.947	33.217	1.00	7.45	6	ATOM	401	HE2	GLN	A	49	40.489	52.278	30.487	1.00	5.00	7
349	C	PR	A	42	33.861	40.056	33.685	1.00	7.06	6	ATOM	402	C	ASP	A	49	41.929	47.121	31.006	1.00	9.30	6
350	O	PR	A	42	34.481	40.819	32.931	1.00	6.95	6	ATOM	403	O	GLN	A	49	40.774	46.745	30.647	1.00	9.52	8
351	H	ALA	A	43	32.875	40.536	34.452	1.00	6.53	7	ATOM	404	H	SER	A	50	43.038	46.690	30.424	1.00	9.20	7
352	CA	ALA	A	43	32.477	41.937	34.481	1.00	6.39	6	ATOM	405	CA	SER	A	50	42.992	45.763	29.281	1.00	9.33	6
353	CB	ALA	A	43	30.968	41.991	34.756	1.00	5.80	6	ATOM	406	CB	SER	A	50	44.173	46.116	28.346	1.00	11.13	6
354	C	ALA	A	43	33.131	42.845	35.529	1.00	6.36	6	ATOM	407	CG	SER	A	50	45.417	45.891	29.000	1.00	14.96	8
355	O	ALA	A	43	32.847	44.042	35.582	1.00	6.42	8	ATOM	408	C	SER	A	50	42.924	44.272	29.626	1.00	8.88	6
356	H	THR	A	44	33.995	42.333	38.394	1.00	6.22	7	ATOM	409	O	SER	A	50	42.810	43.409	28.738	1.00	8.96	8
357	CA	THR	A	44	34.637	43.052	37.465	1.00	6.10	6	ATOM	410	H	ASP	A	51	42.910	43.891	30.881	1.00	8.41	7
358	CB	THR	A	44	34.455	42.266	38.819	1.00	6.31	6	ATOM	411	CA	ASP	A	51	42.812	42.467	31.211	1.00	7.98	6
359	CO	THR	A	44	34.381	40.781	38.551	1.00	6.51	6	ATOM	412	CB	ASP	A	51	43.050	42.803	32.729	1.00	7.44	6
360	CD1	THR	A	44	35.538	40.086	38.145	1.00	6.67	6	ATOM	413	CG	ASP	A	51	43.044	40.822	33.178	1.00	8.58	6
361	CE1	THR	A	44	35.472	38.732	37.848	1.00	6.66	6	ATOM	414	CD1	ASP	A	51	44.049	40.115	32.869	1.00	8.63	8
362	CD2	THR	A	44	33.600	40.071	38.613	1.00	6.52	6	ATOM	415	CD2	ASP	A	51	43.992	40.399	33.679	1.00	8.06	8
363	CE2	THR	A	44	33.108	38.722	38.301	1.00	6.55	6	ATOM	416	C	ASP	A	51	43.469	41.932	30.766	1.00	7.80	6
364	CE3	THR	A	44	34.276	38.073	37.917	1.00	6.98	6	ATOM	417	O	ASP	A	51	40.441	42.613	30.990	1.00	7.78	8
365	CH	THR	A	44	34.599	36.729	37.588	1.00	7.43	8	ATOM	418	H	ASN	A	52	41.330	40.729	30.217	1.00	7.56	7
366	C	THR	A	44	36.060	43.413	37.075	1.00	5.99	6	ATOM	419	CA	ASN	A	52	40.060	40.182	29.847	1.00	7.47	6
367	O	THR	A	44	36.682	42.965	36.097	1.00	5.98	8	ATOM	420	CB	ASN	A	52	40.175	30.887	29.057	1.00	9.45	6
368	H	LYS	A	45	36.556	44.410	37.815	1.00	5.93	7	ATOM	421	CG	ASN	A	52	40.562	39.187	27.620	1.00	12.85	6
369	CA	LYS	A	45	37.865	45.083	37.587	1.00	5.73	6	ATOM	422	CD1	ASN	A	52	40.516	40.341	27.167	1.00	15.76	8
370	CB	LYS	A	45	38.033	46.160	38.580	1.00	5.00	6	ATOM	423	CD2	ASN	A	52	40.979	38.239	26.786	1.00	12.70	7
371	CG	LYS	A	45	39.192	47.127	38.251	1.00	5.00	6	ATOM	424	C	ASN	A	52	39.166	39.629	31.071	1.00	7.16	6

425	ASH A	52	38.007	39.399	30.782	1.00	7.11	8	
426	N	GLY A	53	39.652	39.949	32.309	1.00	6.67	7
427	CA	GLY A	53	38.832	39.609	33.457	1.00	6.52	6
428	C	GLY A	53	39.262	38.324	34.154	1.00	6.62	6
429	D	GLY A	53	38.726	38.021	35.199	1.00	6.86	8
430	N	GLY A	54	40.227	37.563	33.548	1.00	6.28	7
431	CA	GLY A	54	40.722	36.331	34.179	1.00	5.98	6
432	CH	GLY A	54	41.027	35.227	33.116	1.00	6.08	6
433	C	GLY A	54	39.720	34.834	32.427	1.00	5.99	6
434	CE1	GLY A	54	39.481	35.232	31.108	1.00	6.46	6
435	CE2	GLY A	54	38.251	34.920	30.492	1.00	6.68	6
436	CE3	GLY A	54	38.700	33.088	31.000	1.00	5.97	6
437	CE2	GLY A	54	37.474	33.657	32.517	1.00	6.05	6
438	C2	GLY A	54	37.282	34.399	31.182	1.00	6.50	6
439	CH	GLY A	54	36.083	33.928	30.558	1.00	6.69	8
440	C	GLY A	54	41.879	36.949	35.145	1.00	5.76	6
441	C	GLY A	54	42.441	35.853	35.818	1.00	5.63	8
442	N	GLY A	55	42.237	37.799	35.429	1.00	5.53	7
443	CA	GLY A	55	43.226	38.205	36.438	1.00	5.64	6
444	C	GLY A	55	42.464	39.315	37.256	1.00	5.59	6
445	D	GLY A	55	42.818	40.499	37.213	1.00	5.60	8
446	N	PRO A	56	41.410	38.876	37.946	1.00	5.20	7
447	CD	PRO A	56	40.952	37.502	38.113	1.00	5.03	6
448	CA	PRO A	56	40.567	39.757	38.732	1.00	5.12	6
449	CG	PRO A	56	39.282	38.948	39.083	1.00	5.13	6
450	CG	PRO A	56	39.914	37.555	39.212	1.00	5.03	6
451	C	PRO A	56	41.189	40.355	39.998	1.00	5.03	6
452	D	PRO A	56	41.728	39.671	40.862	1.00	5.00	8
453	N	GLY A	57	41.081	41.640	40.099	1.00	5.00	7
454	CA	GLY A	57	41.499	42.474	41.207	1.00	5.00	6
455	CG	GLY A	57	42.042	43.842	40.780	1.00	5.45	6
456	C	GLY A	57	42.261	44.833	41.860	1.00	6.29	6
457	CD1	GLY A	57	43.330	44.834	42.730	1.00	6.86	6
458	CE1	GLY A	57	43.921	45.499	43.810	1.00	7.20	6
459	CE2	GLY A	57	41.621	45.913	42.014	1.00	6.52	6
460	CE2	GLY A	57	41.634	44.788	43.085	1.00	6.96	6
461	C2	GLY A	57	42.669	46.566	43.963	1.00	7.37	6
462	CH	GLY A	57	42.835	47.431	45.036	1.00	7.85	8
463	C	GLY A	57	40.372	42.681	42.201	1.00	5.00	6
464	D	GLY A	57	40.546	42.347	43.362	1.00	5.00	8
465	N	ASP A	58	39.210	43.212	41.826	1.00	5.00	7
466	CA	ASP A	58	38.134	42.465	42.771	1.00	5.00	6
467	CG	ASP A	58	38.136	44.990	43.088	1.00	5.00	6
468	CG	ASP A	58	37.210	45.478	44.152	1.00	5.00	6
469	CE1	ASP A	58	36.550	44.681	44.829	1.00	5.00	8
470	CE2	ASP A	58	36.995	46.702	44.368	1.00	5.00	8
471	C	ASP A	58	36.013	42.974	42.250	1.00	5.00	6
472	D	ASP A	58	36.224	43.643	41.379	1.00	5.00	8
473	N	LEU A	59	36.258	41.917	42.874	1.00	5.00	7
474	CA	LEU A	59	34.967	41.399	42.626	1.00	5.00	6
475	CG	LEU A	59	34.696	40.040	43.128	1.00	6.31	6
476	CG	LEU A	59	35.782	38.942	42.885	1.00	8.19	6
477	CD1	LEU A	59	35.479	37.701	43.725	1.00	7.46	6
478	CD2	LEU A	59	35.980	38.571	43.423	1.00	6.96	6
479	C	LEU A	59	33.750	42.311	42.650	1.00	5.05	6
480	N	LEU A	59	32.644	42.112	42.100	1.00	5.00	8
481	W	LEU A	60	33.921	43.352	43.480	1.00	5.25	7
482	CA	LEU A	60	32.804	44.266	43.786	1.00	5.52	6
483	CG	LEU A	60	32.811	44.611	45.271	1.00	5.24	6
484	CG	LEU A	60	32.214	43.597	46.274	1.00	5.38	6
485	CD1	LEU A	60	33.101	42.761	46.929	1.00	5.85	6
486	CE1	LEU A	60	32.646	41.833	47.866	1.00	5.89	6
487	CD2	LEU A	60	30.855	43.441	48.441	1.00	5.22	6
488	CE2	LEU A	60	30.359	42.520	47.333	1.00	5.60	6
489	C2	LEU A	60	31.255	41.742	48.063	1.00	6.27	6
490	CH	LEU A	60	30.867	40.764	48.957	1.00	6.71	8
491	C	LEU A	60	32.888	45.540	48.937	1.00	5.77	6
492	D	LEU A	60	32.117	46.467	43.158	1.00	6.16	8
493	N	ASP A	61	33.824	45.690	42.052	1.00	5.53	7
494	CA	ASP A	61	33.963	46.831	41.196	1.00	5.82	6
495	CG	ASP A	61	35.395	47.325	41.096	1.00	5.00	6
496	CG	ASP A	61	35.635	48.569	40.256	1.00	5.28	6
497	CD1	ASP A	61	34.717	49.013	39.448	1.00	6.54	8
498	CD2	ASP A	61	33.455	46.590	39.790	1.00	6.20	8
499	C	ASP A	61	34.313	45.844	39.045	1.00	6.25	8
500	N	LEU A	62	32.228	46.608	39.374	1.00	6.27	7
501	CA	LEU A	62	31.732	46.208	38.072	1.00	6.89	6
502	CG	LEU A	62	30.242	45.815	38.193	1.00	7.43	6
503	CG	LEU A	62	29.864	44.704	39.231	1.00	9.12	6
504	CD1	LEU A	62	28.372	44.443	39.402	1.00	6.08	6
505	CD2	LEU A	62	30.514	43.337	38.889	1.00	9.37	6
506	C	LEU A	62	31.934	47.317	37.053	1.00	7.56	6
507	N	GLY A	63	31.256	47.422	36.044	1.00	7.76	8
508	CG	GLY A	63	32.908	48.248	37.209	1.00	7.95	7
509	CA	GLY A	63	33.126	49.358	36.307	1.00	7.98	6
510	C	GLY A	63	32.529	50.656	36.862	1.00	6.19	6
511	CG	GLY A	63	31.954	51.388	36.084	1.00	7.99	8
512	N	GLY A	64	32.685	50.974	38.143	1.00	8.78	7
513	CA	GLY A	64	32.154	52.244	38.659	1.00	9.55	6
514	CG	GLY A	64	30.916	51.062	40.517	1.00	10.66	6
515	CG	GLY A	64	29.829	50.986	41.287	1.00	13.63	6
516	CD	GLY A	64	29.203	49.959	41.856	1.00	16.12	8
517	CE1	GLY A	64	28.864	51.950	41.397	1.00	15.85	8
518	CE2	GLY A	64	33.046	52.958	39.664	1.00	9.91	6
519	C	GLY A	64	32.691	53.987	40.243	1.00	9.88	8
520	N	PHE A	65	35.172	52.891	49.936	1.00	10.39	7
521	CA	PHE A	65	34.212	52.363	49.936	1.00	10.39	7
522	CG	PHE A	65	35.412	51.981	42.114	1.00	9.02	6
523	CG	PHE A	65	34.151	51.862	42.878	1.00	8.75	6
524	CD	PHE A	65	33.541	50.420	42.879	1.00	7.83	6
525	CE1	PHE A	65	33.508	52.662	43.617	1.00	7.65	6
526	CE2	PHE A	65	32.339	50.164	43.499	1.00	6.31	6
527	C	PHE A	65	32.322	52.686	44.296	1.00	6.18	6
528	N	PHE A	65	31.739	51.48	46.248	1.00	5.83	6

637	ATOM	637	R	SEB	A	79	26.749	50.759	34.578	1.00	9.32	7
638	ATOM	638	CA	SEB	A	79	25.401	51.141	34.086	1.00	9.71	6
639	ATOM	639	CB	SEB	A	79	25.190	52.607	33.480	1.00	12.14	6
640	ATOM	640	CG	SEB	A	79	25.960	53.338	33.438	1.00	15.84	6
641	ATOM	641	C	SEB	A	79	25.262	50.703	32.644	1.00	9.79	6
642	ATOM	642	D	SEB	A	79	24.142	50.254	32.312	1.00	10.15	7
643	ATOM	643	E	SEB	A	80	26.291	50.655	31.614	1.00	9.56	7
644	ATOM	644	CA	SEB	A	80	26.160	50.128	30.452	1.00	9.39	6
645	ATOM	645	CB	SEB	A	80	27.429	50.452	29.373	1.00	10.04	6
646	ATOM	646	CG	SEB	A	80	27.546	51.928	29.728	1.00	11.54	6
647	ATOM	647	CD	SEB	A	80	28.902	52.167	28.769	1.00	14.36	6
648	ATOM	648	CE	SEB	A	80	29.881	51.408	28.015	1.00	15.28	8
649	ATOM	649	CE2	SEB	A	80	29.051	51.186	28.075	1.00	16.22	8
650	ATOM	650	C	SEB	A	80	25.853	48.629	30.476	1.00	9.05	6
651	ATOM	651	D	SEB	A	80	25.005	48.179	29.720	1.00	8.72	8
652	ATOM	652	E	SEB	A	81	26.441	47.873	31.394	1.00	9.09	7
653	ATOM	653	CA	SEB	A	81	26.145	46.428	31.534	1.00	9.12	6
654	ATOM	654	CB	SEB	A	81	27.188	45.716	32.385	1.00	8.24	6
655	ATOM	655	CG	SEB	A	81	26.866	44.272	32.843	1.00	8.68	6
656	ATOM	656	CD	SEB	A	81	26.744	43.229	31.738	1.00	7.74	6
657	ATOM	657	CE	SEB	A	81	27.903	43.841	33.771	1.00	9.60	6
658	ATOM	658	C	SEB	A	81	24.710	45.226	32.053	1.00	9.19	6
659	ATOM	659	D	SEB	A	81	23.952	45.386	31.515	1.00	8.94	6
660	ATOM	660	E	SEB	A	82	24.247	47.005	33.042	1.00	9.33	7
661	ATOM	661	CA	SEB	A	82	22.853	46.834	33.479	1.00	9.81	6
662	ATOM	662	CB	SEB	A	82	22.588	47.739	34.681	1.00	11.55	6
663	ATOM	663	CG	SEB	A	82	23.288	47.105	35.901	1.00	14.03	6
664	ATOM	664	CD	SEB	A	82	23.239	47.993	37.132	1.00	14.62	6
665	ATOM	665	CE	SEB	A	82	23.497	49.180	36.990	1.00	15.76	8
666	ATOM	666	CE2	SEB	A	82	22.947	47.300	38.266	1.00	14.70	7
667	ATOM	667	C	SEB	A	82	21.878	47.108	32.358	1.00	10.18	6
668	ATOM	668	D	SEB	A	82	20.854	46.455	32.247	1.00	10.30	6
669	ATOM	669	E	SEB	A	83	22.106	48.088	31.501	1.00	10.58	7
670	ATOM	670	CA	SEB	A	83	21.281	48.355	30.517	1.00	11.05	6
671	ATOM	671	CB	SEB	A	83	21.631	49.619	29.514	1.00	15.09	6
672	ATOM	672	CG	SEB	A	83	21.228	50.893	30.246	1.00	18.79	6
673	ATOM	673	CD	SEB	A	83	20.404	50.950	31.175	1.00	18.59	8
674	ATOM	674	CE	SEB	A	83	21.832	51.914	29.841	1.00	22.13	8
675	ATOM	675	C	SEB	A	83	21.439	47.203	29.307	1.00	10.81	6
676	ATOM	676	D	SEB	A	83	20.391	46.942	28.751	1.00	11.02	8
677	ATOM	677	E	SEB	A	84	22.562	46.574	29.048	1.00	10.37	7
678	ATOM	678	CA	SEB	A	84	22.630	45.461	28.120	1.00	10.32	6
679	ATOM	679	CB	SEB	A	84	24.057	45.019	27.847	1.00	7.64	6
680	ATOM	680	CG	SEB	A	84	21.758	46.332	28.688	1.00	10.46	6
681	ATOM	681	CD	SEB	A	84	20.988	43.692	27.939	1.00	10.32	8
682	ATOM	682	CE	SEB	A	85	21.828	44.045	29.995	1.00	10.47	7
683	ATOM	683	CA	SEB	A	85	21.836	42.985	30.642	1.00	10.46	6
684	ATOM	684	CB	SEB	A	85	21.501	42.710	32.116	1.00	9.71	6
685	ATOM	685	CE2	SEB	A	85	20.474	41.875	32.906	1.00	6.40	6
686	ATOM	686	CE1	SEB	A	85	22.921	42.132	32.080	1.00	9.01	6
687	ATOM	687	C	SEB	A	85	21.664	42.092	33.399	1.00	10.12	6
688	ATOM	688	D	SEB	A	85	19.543	43.282	30.565	1.00	10.65	6
689	ATOM	689	E	SEB	A	85	18.768	42.348	30.313	1.00	10.41	8

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743	743	N	VAL A 93	15.886	36.642	24.969	1.00	16.55	7	ATOM	746	O	VAL A 99	34.461	31.987	37.850	1.00	6.66	8
744	744	CA	VAL A 93	17.213	36.038	28.853	1.00	15.28	6	ATOM	747	N	VAL A 100	35.082	34.017	38.489	1.00	6.60	7
745	745	CA	VAL A 93	18.120	36.688	25.785	1.00	12.97	6	ATOM	748	CA	VAL A 100	36.487	33.766	38.594	1.00	6.45	6
746	746	CB1	VAL A 93	19.467	36.021	25.569	1.00	11.55	6	ATOM	749	CB	VAL A 100	37.273	34.786	37.735	1.00	6.69	6
747	747	CB2	VAL A 93	17.378	36.751	28.453	1.00	12.38	6	ATOM	800	CB1	VAL A 100	38.728	34.308	37.697	1.00	6.74	6
748	748	C	VAL A 93	17.771	36.161	28.256	1.00	14.48	6	ATOM	801	CB2	VAL A 100	36.761	34.893	36.314	1.00	6.94	6
749	749	O	VAL A 93	17.736	37.220	28.829	1.00	14.36	8	ATOM	802	C	VAL A 100	36.930	33.803	40.041	1.00	6.61	6
750	750	N	GLA A 94	18.211	35.007	28.742	1.00	13.97	7	ATOM	803	O	VAL A 100	37.308	34.866	40.566	1.00	6.72	8
751	751	CA	GLA A 94	18.792	34.812	30.065	1.00	13.10	6	ATOM	804	N	LEU A 101	36.882	32.651	40.724	1.00	6.41	7
752	752	CB	GLA A 94	18.642	33.375	30.542	1.00	13.42	6	ATOM	805	CA	LEU A 101	37.189	32.537	42.133	1.00	6.10	6
753	753	CO	GLA A 94	17.183	33.283	30.919	1.00	16.17	6	ATOM	806	CB	LEU A 101	36.617	31.716	42.731	1.00	7.20	6
754	754	CO	GLA A 94	17.047	31.820	31.552	1.00	19.51	6	ATOM	807	CG	LEU A 101	34.663	32.579	42.645	1.00	8.90	6
755	755	CE1	GLA A 94	17.710	30.855	31.198	1.00	11.76	8	ATOM	808	CO1	LEU A 101	33.657	31.509	43.300	1.00	9.60	6
756	756	HE2	GLA A 94	16.266	31.683	32.559	1.00	21.21	7	ATOM	809	CO2	LEU A 101	34.726	33.873	43.244	1.00	7.63	6
757	757	C	GLA A 94	20.275	33.223	30.003	1.00	12.28	6	ATOM	810	C	LEU A 101	38.456	31.843	42.579	1.00	5.96	6
758	758	O	GLA A 94	20.882	35.311	28.935	1.00	12.02	8	ATOM	811	O	LEU A 101	38.672	31.740	43.782	1.00	6.02	8
759	759	N	VAL A 95	20.772	35.576	31.218	1.00	11.32	7	ATOM	812	N	ASP A 102	39.260	31.326	41.676	1.00	5.73	7
760	760	CA	VAL A 95	22.146	36.030	31.272	1.00	10.46	6	ATOM	813	CA	ASP A 102	40.471	30.629	42.025	1.00	5.58	6
761	761	CB	VAL A 95	22.215	37.553	31.568	1.00	11.92	6	ATOM	814	CB	ASP A 102	40.963	29.889	40.727	1.00	5.00	6
762	762	CG1	VAL A 95	23.646	38.014	31.735	1.00	12.83	6	ATOM	815	CG	ASP A 102	42.327	29.247	40.912	1.00	5.00	6
763	763	CG2	VAL A 95	21.591	38.367	30.411	1.00	12.21	6	ATOM	816	CO1	ASP A 102	42.309	28.218	41.608	1.00	5.00	8
764	764	C	VAL A 95	22.942	35.249	32.302	1.00	9.65	6	ATOM	817	CO2	ASP A 102	43.493	29.653	40.442	1.00	5.00	7
765	765	D	VAL A 95	22.559	35.259	33.483	1.00	9.73	8	ATOM	818	C	ASP A 102	41.580	31.490	42.620	1.00	5.69	6
766	766	N	THR A 96	26.034	36.613	31.857	1.00	8.90	7	ATOM	819	O	ASP A 102	42.261	31.045	43.593	1.00	6.11	8
767	767	CA	THR A 96	24.920	33.882	32.786	1.00	8.34	6	ATOM	820	N	HIS A 103	41.853	32.670	42.103	1.00	5.60	7
768	768	CB	THR A 96	25.217	32.512	32.267	1.00	8.31	6	ATOM	821	CA	HIS A 103	42.935	33.528	42.506	1.00	5.59	6
769	769	CG	THR A 96	24.055	31.583	31.987	1.00	8.37	6	ATOM	822	CB	HIS A 103	44.089	33.287	41.687	1.00	6.54	6
770	770	CO1	THR A 96	24.298	30.500	31.130	1.00	8.46	6	ATOM	823	CG	HIS A 103	43.645	33.442	40.043	1.00	7.70	6
771	771	CE1	THR A 96	23.255	29.463	30.831	1.00	8.38	6	ATOM	824	CO2	HIS A 103	43.560	34.512	39.230	1.00	6.52	6
772	772	CE2	THR A 96	22.797	31.752	32.491	1.00	8.19	6	ATOM	825	CO1	HIS A 103	43.187	32.341	39.282	1.00	9.01	7
773	773	CE2	THR A 96	21.742	30.928	32.186	1.00	8.05	6	ATOM	826	CE1	HIS A 103	42.794	32.769	38.082	1.00	8.40	6
774	774	C2	THR A 96	22.011	29.854	31.363	1.00	7.94	6	ATOM	827	CE2	HIS A 103	42.993	34.113	38.070	1.00	8.31	7
775	775	OH	THR A 96	21.055	28.940	31.084	1.00	7.64	8	ATOM	828	C	HIS A 103	42.555	34.977	42.419	1.00	5.57	6
776	776	C	THR A 96	26.218	34.655	33.000	1.00	8.00	8	ATOM	829	O	HIS A 103	41.478	35.229	41.899	1.00	5.20	8
777	777	O	THR A 96	26.855	35.017	32.005	1.00	7.99	8	ATOM	830	N	LYS A 104	43.438	35.861	42.914	1.00	5.83	7
778	778	N	GLY A 97	26.624	35.919	34.243	1.00	7.85	7	ATOM	831	CA	LYS A 104	42.228	37.313	42.871	1.00	6.01	6
779	779	CA	GLY A 97	27.818	35.871	34.578	1.00	7.64	6	ATOM	832	CB	LYS A 104	42.938	37.971	44.213	1.00	8.00	6
780	780	C	GLY A 97	29.038	34.754	34.756	1.00	7.84	6	ATOM	833	CG	LYS A 104	41.748	37.393	44.978	1.00	8.52	6
781	781	O	GLY A 97	28.950	33.655	35.307	1.00	7.51	8	ATOM	834	CO	LYS A 104	41.373	38.374	46.133	1.00	9.80	6
782	782	N	ASP A 98	30.194	35.231	35.871	1.00	7.87	7	ATOM	835	CE	LYS A 104	40.973	39.768	45.746	1.00	8.97	6
783	783	CA	ASP A 98	31.453	34.489	34.482	1.00	8.04	6	ATOM	836	H2	LYS A 104	39.514	39.723	45.383	1.00	8.50	7
784	784	CB	ASP A 98	32.546	34.944	33.523	1.00	7.77	6	ATOM	837	O	LYS A 104	44.489	37.894	42.278	1.00	6.11	6
785	785	C2	ASP A 98	33.452	33.828	33.077	1.00	7.80	6	ATOM	838	O	LYS A 104	45.526	37.371	42.649	1.00	6.50	8
786	786	CO1	ASP A 98	33.916	33.045	33.920	1.00	8.28	8	ATOM	839	N	ALA A 105	44.501	38.896	41.451	1.00	5.96	7
787	787	CO2	ASP A 98	31.791	33.741	31.896	1.00	8.14	8	ATOM	840	CA	ALA A 105	45.699	39.429	40.846	1.00	6.18	6
788	788	C	ASP A 98	31.668	34.668	35.953	1.00	7.80	6	ATOM	841	CB	ALA A 105	45.660	39.063	39.341	1.00	5.88	6
789	789	O	ASP A 98	31.644	35.739	36.518	1.00	7.83	8	ATOM	842	C	ALA A 105	45.785	40.943	41.031	1.00	6.37	6
790	790	N	VAL A 99	32.333	33.601	36.602	1.00	7.67	7	ATOM	843	O	GLY A 106	44.741	41.578	41.199	1.00	6.24	8
791	791	CA	VAL A 99	32.708	33.576	38.035	1.00	7.25	6	ATOM	844	N	GLY A 106	46.958	41.584	41.044	1.00	6.40	7
792	792	CB	VAL A 99	31.742	32.652	38.791	1.00	8.70	6	ATOM	845	CA	GLY A 106	47.040	43.001	41.190	1.00	6.40	6
793	793	CG1	VAL A 99	32.193	32.306	40.195	1.00	9.79	6	ATOM	846	C	GLY A 106	47.006	43.411	42.573	1.00	7.01	6
794	794	CG2	VAL A 99	30.366	33.362	38.885	1.00	9.90	6	ATOM	847	O	GLY A 106	46.524	44.756	42.659	1.00	6.76	8
795	795	C	VAL A 99	34.155	33.123	38.148	1.00	6.81	6	ATOM	848	N	ALA A 107	47.489	42.945	43.637	1.00	7.49	7

849	EA	ALA	A 107	47.462	43.434	44.979	1.00	7.87	6	ATOM	902	C	THR	A 114	56.563	31.547	54.495	1.00	11.69	6
850	CB	ALA	A 107	48.271	42.572	45.920	1.00	5.59	6	ATOM	903	O	THR	A 114	55.355	31.265	54.457	1.00	11.32	8
851	C	ALA	A 107	48.855	44.842	46.970	1.00	8.91	6	ATOM	904	N	ALA	A 115	57.429	31.042	53.643	1.00	11.64	7
852	O	ALA	A 107	48.875	45.204	44.128	1.00	8.95	8	ATOM	905	CA	ALA	A 115	57.034	30.048	52.638	1.00	11.55	6
853	N	ASP	A 108	47.647	45.849	45.934	1.00	9.17	7	ATOM	906	CB	ALA	A 115	56.825	30.894	51.357	1.00	10.80	6
854	CA	ASP	A 108	48.106	47.011	46.130	1.00	9.77	6	ATOM	907	C	ALA	A 115	59.215	28.947	52.343	1.00	11.45	6
855	CB	ASP	A 108	47.118	47.666	47.155	1.00	10.59	6	ATOM	908	O	ALA	A 115	59.215	29.073	52.688	1.00	11.41	8
856	CO	ASP	A 108	45.718	47.703	44.582	1.00	10.42	6	ATOM	909	N	VAL	A 116	57.641	27.868	51.657	1.00	11.33	7
857	COO	ASP	A 108	44.585	47.094	44.851	1.00	10.41	8	ATOM	910	CA	VAL	A 116	58.513	26.814	51.184	1.00	11.10	6
858	COO	ASP	A 108	45.580	48.455	45.604	1.00	12.47	8	ATOM	911	CB	VAL	A 116	58.338	25.435	51.815	1.00	12.01	6
859	C	ASP	A 108	49.530	47.044	46.683	1.00	10.18	6	ATOM	912	CO	VAL	A 116	58.978	25.449	53.208	1.00	12.23	6
860	O	ASP	A 108	50.281	48.011	46.478	1.00	10.34	8	ATOM	913	CO	VAL	A 116	56.882	24.978	51.873	1.00	11.15	6
861	N	ALA	A 109	49.958	46.023	47.436	1.00	10.17	7	ATOM	914	C	VAL	A 116	56.250	26.642	49.456	1.00	10.95	6
862	CA	ALA	A 109	51.373	45.970	48.023	1.00	10.21	6	ATOM	915	O	VAL	A 116	57.100	26.960	49.240	1.00	11.03	8
863	CB	ALA	A 109	51.271	46.787	49.322	1.00	10.14	6	ATOM	916	N	GLU	A 117	59.187	26.205	48.856	1.00	10.29	7
864	C	ALA	A 109	51.649	44.553	48.398	1.00	10.56	6	ATOM	917	CA	GLU	A 117	58.932	25.898	47.465	1.00	10.06	6
865	O	ALA	A 109	50.836	43.629	48.473	1.00	10.49	8	ATOM	918	CB	GLU	A 117	60.201	25.861	46.625	1.00	11.90	6
866	N	THR	A 110	52.966	44.438	48.710	1.00	10.81	7	ATOM	919	CG	GLU	A 117	60.905	27.201	46.773	1.00	14.30	6
867	CA	THR	A 110	53.504	43.168	49.132	1.00	11.01	6	ATOM	920	CD	GLU	A 117	62.245	27.143	46.070	1.00	16.13	6
868	CB	THR	A 110	54.958	42.954	48.785	1.00	11.26	6	ATOM	921	OE	GLU	A 117	62.515	28.342	45.175	1.00	16.80	8
869	COO	THR	A 110	55.741	43.988	49.294	1.00	11.79	8	ATOM	922	OE	GLU	A 117	63.067	28.004	46.366	1.00	17.32	6
870	COO	THR	A 110	55.196	43.053	47.209	1.00	11.23	6	ATOM	923	C	GLU	A 117	58.354	24.480	47.369	1.00	9.47	8
871	C	THR	A 110	53.465	43.091	50.843	1.00	11.37	6	ATOM	924	O	GLU	A 117	58.596	23.656	48.258	1.00	9.47	8
872	O	THR	A 110	53.369	44.102	51.351	1.00	11.33	8	ATOM	925	N	VAL	A 118	57.623	24.157	46.316	1.00	9.40	7
873	N	GLU	A 111	53.477	41.851	51.165	1.00	11.70	7	ATOM	926	CA	VAL	A 118	56.987	22.802	46.152	1.00	9.25	6
874	CA	GLU	A 111	53.527	41.584	52.566	1.00	11.89	6	ATOM	927	CB	VAL	A 118	55.556	23.243	46.543	1.00	10.55	6
875	CB	GLU	A 111	52.223	40.870	53.035	1.00	10.98	6	ATOM	928	CO	VAL	A 118	54.529	23.164	45.421	1.00	9.52	6
876	CO	GLU	A 111	51.153	41.995	53.103	1.00	13.15	6	ATOM	929	CO	VAL	A 118	55.081	22.664	47.855	1.00	10.49	6
877	CO	GLU	A 111	49.812	41.428	53.483	1.00	14.55	6	ATOM	930	C	VAL	A 118	57.360	22.305	44.765	1.00	9.31	6
878	OE	GLU	A 111	49.365	40.456	52.823	1.00	14.72	8	ATOM	931	O	VAL	A 118	57.660	23.097	43.823	1.00	9.23	8
879	OE	GLU	A 111	49.218	41.958	54.436	1.00	15.89	8	ATOM	932	CA	ASH	A 119	57.381	20.998	44.492	1.00	8.84	7
880	O	GLU	A 111	54.697	40.516	52.799	1.00	12.41	6	ATOM	933	N	ASH	A 119	57.701	20.503	43.206	1.00	8.20	6
881	O	GLU	A 111	55.011	39.715	51.878	1.00	12.22	8	ATOM	934	CB	ASH	A 119	57.911	18.914	43.534	1.00	7.82	6
882	N	ASP	A 112	55.284	40.485	53.081	1.00	12.71	7	ATOM	935	CG	ASH	A 119	58.248	18.097	42.289	1.00	8.10	6
883	CA	ASP	A 112	56.344	39.543	54.283	1.00	13.23	6	ATOM	936	CO	ASH	A 119	58.084	18.834	41.177	1.00	7.16	8
884	CB	ASP	A 112	57.290	39.993	55.380	1.00	18.18	6	ATOM	937	CO	ASH	A 119	58.706	16.848	42.386	1.00	6.98	7
885	CO	ASP	A 112	58.008	41.297	55.120	1.00	21.75	6	ATOM	938	C	ASH	A 119	56.553	20.692	42.242	1.00	7.98	6
886	COO	ASP	A 112	58.435	41.747	54.039	1.00	23.40	8	ATOM	939	O	ASH	A 119	55.382	20.314	42.482	1.00	7.64	8
887	COO	ASP	A 112	58.189	42.024	56.128	1.00	24.60	8	ATOM	940	N	PRO	A 120	56.813	21.326	41.094	1.00	8.04	7
888	C	ASP	A 112	55.666	38.250	54.730	1.00	13.29	6	ATOM	941	CO	PRO	A 120	58.207	21.793	40.728	1.00	8.00	6
889	O	ASP	A 112	54.808	38.272	55.608	1.00	13.60	8	ATOM	942	CA	PRO	A 120	55.849	21.704	40.088	1.00	8.27	6
890	N	VAL	A 113	56.015	37.098	54.153	1.00	13.04	7	ATOM	943	CG	PRO	A 120	56.609	22.404	38.938	1.00	8.21	6
891	CA	VAL	A 113	55.391	35.819	54.410	1.00	12.72	6	ATOM	944	CO	PRO	A 120	57.980	22.618	39.530	1.00	8.16	6
892	CB	VAL	A 113	54.466	35.495	53.295	1.00	13.86	6	ATOM	945	C	PRO	A 120	55.032	20.526	39.601	1.00	8.65	8
893	CO	VAL	A 113	53.658	34.192	53.418	1.00	14.55	6	ATOM	946	O	PRO	A 120	53.850	20.633	39.275	1.00	8.69	8
894	COO	VAL	A 113	53.423	36.541	52.806	1.00	13.68	6	ATOM	947	N	ALA	A 121	55.648	19.337	39.540	1.00	9.00	7
895	C	VAL	A 113	55.407	34.721	54.511	1.00	12.52	6	ATOM	948	CA	ALA	A 121	56.977	18.104	39.122	1.00	9.39	6
896	O	VAL	A 113	57.412	34.748	53.765	1.00	12.66	8	ATOM	949	CB	ALA	A 121	55.976	17.215	38.324	1.00	9.49	6
897	N	THR	A 114	56.218	33.728	55.355	1.00	12.21	7	ATOM	950	C	ALA	A 121	54.374	17.315	40.267	1.00	9.46	6
898	CA	THR	A 114	57.167	32.595	55.443	1.00	11.87	6	ATOM	951	O	ALA	A 121	53.664	16.327	40.066	1.00	9.60	8
899	CB	THR	A 114	57.212	31.941	56.809	1.00	12.74	6	ATOM	952	N	ASH	A 122	54.624	17.656	41.537	1.00	9.45	7
900	COO	THR	A 114	57.602	32.955	57.761	1.00	14.06	8	ATOM	953	CA	ASH	A 122	56.040	16.971	42.679	1.00	9.32	6
901	COO	THR	A 114	58.195	30.781	56.909	1.00	10.83	6	ATOM	954	CB	ASH	A 122	54.681	15.602	43.207	1.00	10.30	6

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AT04	955	CG	ASH A 122	54.089	15.047	44.188	1.00	13.39	6	ATOM	1008	C	SE8 A 128	62.620	23.784	51.617	1.00	18.11	6
AT04	956	003	ASH A 122	53.085	15.591	44.786	1.00	13.50	8	ATOM	1009	O	SE8 A 128	61.642	23.254	52.161	1.00	17.96	8
AT04	957	W02	ASH A 122	54.211	13.733	44.357	1.00	16.10	7	ATOM	1010	H	SE8 A 129	63.523	24.444	52.326	1.00	18.90	7
AT04	958	C	ASH A 122	53.936	18.050	43.762	1.00	9.22	6	ATOM	1011	CA	GLU A 129	63.393	24.747	53.735	1.00	19.85	6
AT04	959	O	ASH A 122	54.881	18.130	44.566	1.00	9.82	8	ATOM	1012	CB	GLU A 129	64.794	24.360	55.817	1.00	27.78	6
AT04	960	H	ASH A 123	52.869	18.855	43.722	1.00	9.27	7	ATOM	1013	CG	GLU A 129	65.311	22.937	55.587	1.00	40.42	6
AT04	961	CA	ARG A 123	52.764	19.983	44.486	1.00	9.33	6	ATOM	1014	CD	GLU A 129	66.375	22.844	54.891	1.00	43.73	6
AT04	962	CB	ARG A 123	51.875	20.989	44.227	1.00	7.86	6	ATOM	1015	OE1	GLU A 129	64.637	21.983	56.055	1.00	42.88	6
AT04	963	CG	ARG A 123	52.067	21.746	42.991	1.00	6.67	6	ATOM	1016	OE2	GLU A 129	62.568	26.060	53.737	1.00	19.49	6
AT04	964	CD	ARG A 123	51.513	21.080	41.764	1.00	6.95	6	ATOM	1017	C	GLU A 129	62.573	26.773	52.713	1.00	19.50	6
AT04	965	HE	ARG A 123	51.759	21.959	40.806	1.00	9.73	7	ATOM	1018	O	GLU A 129	61.925	26.390	54.849	1.00	19.52	7
AT04	966	CZ	ARG A 123	50.956	22.937	40.275	1.00	10.25	6	ATOM	1019	H	GLU A 130	61.150	27.812	54.769	1.00	19.43	6
AT04	967	HH1	ARG A 123	49.828	23.054	41.044	1.00	9.79	7	ATOM	1020	CA	GLU A 130	60.090	27.530	55.867	1.00	23.57	6
AT04	968	HH2	ARG A 123	51.000	23.793	39.273	1.00	10.20	7	ATOM	1021	CB	GLU A 130	60.613	27.773	57.215	1.00	26.39	6
AT04	969	C	ARG A 123	52.593	19.557	46.158	1.00	9.23	6	ATOM	1022	CG	GLU A 130	59.542	27.368	58.282	1.00	29.94	6
AT04	970	O	ARG A 123	52.622	20.374	47.085	1.00	8.71	8	ATOM	1023	CD	GLU A 130	59.493	28.140	59.202	1.00	31.34	8
AT04	971	H	ASH A 124	52.408	18.256	46.379	1.00	9.58	7	ATOM	1024	OE1	GLU A 130	58.779	26.388	58.051	1.00	30.50	8
AT04	972	CA	ASH A 124	52.351	17.706	47.712	1.00	10.31	6	ATOM	1025	OE2	GLU A 130	61.988	28.851	54.837	1.00	18.97	6
AT04	973	CB	ASH A 124	51.742	16.299	47.800	1.00	11.34	6	ATOM	1026	C	GLU A 130	63.023	28.894	55.454	1.00	19.04	8
AT04	974	CG	ASH A 124	50.275	16.347	47.455	1.00	14.21	6	ATOM	1027	O	GLU A 130	61.506	29.854	56.117	1.00	17.87	6
AT04	975	HH1	ASH A 124	49.565	17.271	47.867	1.00	14.26	8	ATOM	1028	H	YR A 131	62.186	31.164	54.098	1.00	18.45	7
AT04	976	HH2	ASH A 124	49.887	15.391	46.590	1.00	16.51	7	ATOM	1029	CA	YR A 131	63.336	31.254	53.126	1.00	18.14	6
AT04	977	C	ASH A 124	53.796	17.584	48.243	1.00	10.74	6	ATOM	1030	CB	YR A 131	63.123	31.022	51.656	1.00	18.56	6
AT04	978	O	ASH A 124	53.976	17.342	49.439	1.00	10.85	8	ATOM	1031	CG	YR A 131	62.817	31.915	49.415	1.00	18.78	6
AT04	979	H	GLU A 125	54.872	17.660	47.433	1.00	10.98	7	ATOM	1032	CD	YR A 131	63.053	32.108	50.786	1.00	18.80	6
AT04	980	CA	GLU A 125	56.223	17.549	47.925	1.00	11.21	6	ATOM	1033	OE1	YR A 131	62.856	29.566	49.772	1.00	18.73	6
AT04	981	CB	GLU A 125	57.169	16.823	46.919	1.00	9.50	6	ATOM	1034	OE2	YR A 131	62.773	30.638	48.908	1.00	18.74	6
AT04	982	CG	GLU A 125	58.582	16.600	47.498	1.00	8.17	6	ATOM	1035	CZ	YR A 131	61.150	32.287	53.841	1.00	16.62	8
AT04	983	CD	GLU A 125	59.546	16.199	46.402	1.00	8.01	6	ATOM	1036	DM	YR A 131	59.992	32.053	53.530	1.00	16.72	8
AT04	984	OE1	GLU A 125	59.184	16.310	45.207	1.00	6.56	8	ATOM	1037	O	YR A 131	61.601	33.503	54.011	1.00	16.51	7
AT04	985	HE2	GLU A 125	60.762	15.784	46.738	1.00	6.20	7	ATOM	1038	CA	GLU A 132	60.855	34.718	53.665	1.00	17.10	6
AT04	986	C	GLU A 125	50.871	18.915	48.156	1.00	11.48	6	ATOM	1039	CB	GLU A 132	61.459	35.882	54.723	1.00	22.79	6
AT04	987	O	GLU A 125	50.960	19.609	47.946	1.00	11.44	8	ATOM	1040	H	GLU A 132	60.607	35.969	55.997	1.00	29.13	6
AT04	988	H	GLU A 126	57.355	19.217	49.360	1.00	11.79	7	ATOM	1041	CA	GLU A 132	61.036	34.850	56.918	1.00	33.56	6
AT04	989	CA	GLU A 126	58.093	20.468	49.610	1.00	12.46	6	ATOM	1042	CB	GLU A 132	62.246	34.659	57.308	1.00	37.13	8
AT04	990	CB	GLU A 126	58.042	20.856	51.115	1.00	11.31	6	ATOM	1043	CG	GLU A 132	60.130	33.934	57.337	1.00	34.32	7
AT04	991	CG	GLU A 126	58.589	20.709	51.582	1.00	12.43	6	ATOM	1044	CD	GLU A 132	60.810	35.318	52.481	1.00	35.05	6
AT04	992	CD	GLU A 126	56.371	21.288	52.993	1.00	13.26	6	ATOM	1045	OE1	GLU A 132	61.881	35.620	51.931	1.00	15.27	8
AT04	993	OE1	GLU A 126	57.329	21.471	53.748	1.00	14.22	8	ATOM	1046	OE2	GLU A 132	59.589	35.505	51.972	1.00	13.86	7
AT04	994	OE2	GLU A 126	55.234	21.519	53.374	1.00	14.72	8	ATOM	1047	C	GLU A 132	59.828	35.111	49.631	1.00	12.62	6
AT04	995	C	GLU A 126	59.513	20.293	49.195	1.00	13.18	6	ATOM	1048	O	GLU A 132	59.810	33.787	49.669	1.00	11.38	6
AT04	996	O	GLU A 126	60.198	19.292	49.513	1.00	12.98	8	ATOM	1049	H	GLU A 132	57.374	34.744	49.978	1.00	11.33	6
AT04	997	H	YR A 127	60.065	21.216	48.430	1.00	14.11	7	ATOM	1050	CA	GLU A 133	56.601	33.908	48.958	1.00	11.24	6
AT04	998	CA	YR A 127	61.407	21.048	47.954	1.00	15.19	6	ATOM	1051	CB	GLU A 133	58.652	37.381	50.761	1.00	11.82	6
AT04	999	CB	YR A 127	61.487	21.193	46.420	1.00	16.68	8	ATOM	1052	CG	GLU A 133	58.026	37.593	51.790	1.00	11.18	8
AT04	1000	CG	YR A 127	60.732	22.349	46.071	1.00	15.49	8	ATOM	1053	CD	GLU A 133	58.611	38.192	49.709	1.00	11.41	7
AT04	1001	CZ	YR A 127	60.902	19.957	45.774	1.00	13.94	6	ATOM	1054	OE1	GLU A 133	57.443	40.681	49.331	1.00	12.71	6
AT04	1002	C	YR A 127	62.377	21.993	48.614	1.00	16.26	6	ATOM	1055	C	GLU A 133	59.019	41.223	50.642	1.00	15.80	8
AT04	1003	O	YR A 127	63.952	21.851	48.283	1.00	16.67	8	ATOM	1056	O	GLU A 133	58.652	37.381	50.761	1.00	11.82	6
AT04	1004	H	SE8 A 128	62.015	22.892	49.503	1.00	16.75	7	ATOM	1057	H	YR A 134	58.611	38.192	49.709	1.00	11.41	7
AT04	1005	CA	SE8 A 128	63.000	23.747	50.125	1.00	17.24	6	ATOM	1058	CA	YR A 134	57.737	39.379	49.674	1.00	11.41	6
AT04	1006	CB	SE8 A 128	65.018	25.141	49.511	1.00	15.04	6	ATOM	1059	CB	YR A 134	58.443	40.681	49.331	1.00	12.71	6
AT04	1007	CG	SE8 A 128	61.873	25.859	49.965	1.00	13.39	8	ATOM	1060	CG	YR A 134	59.019	41.223	50.642	1.00	15.80	8

CD

1061	ATOM	CD	LYS A 134	59.998	42.325	50.294	1.00	19.11	6	1114	CG	ARG A 140	45.059	48.594	50.380	1.00	22.69	6
1062	ATOM	CE	LYS A 134	59.652	43.476	51.853	1.00	22.58	6	1115	CD	ARG A 140	45.796	48.583	51.753	1.00	27.78	6
1063	ATOM	H2	LYS A 134	59.863	42.966	52.856	1.00	24.21	7	1116	HE	ARG A 140	47.197	48.785	51.426	1.00	32.35	7
1064	ATOM	C	LYS A 134	56.693	39.066	48.618	1.00	10.75	6	1117	C1	ARG A 140	48.476	48.985	51.487	1.00	34.38	6
1065	ATOM	C	LYS A 134	57.075	38.997	47.439	1.00	10.72	8	1118	WH1	ARG A 140	48.873	49.714	50.421	1.00	34.62	7
1066	ATOM	H	ALA A 135	55.444	38.754	48.593	1.00	10.26	7	1119	WH2	ARG A 140	49.440	48.518	52.329	1.00	34.86	6
1067	ATOM	CA	ALA A 135	54.411	38.356	48.866	1.00	9.82	6	1120	C	ARG A 140	41.765	48.037	49.205	1.00	11.28	6
1068	ATOM	CB	ALA A 135	53.713	37.071	48.552	1.00	8.45	6	1121	O	ARG A 140	40.965	48.699	49.916	1.00	11.54	8
1069	ATOM	C	ALA A 135	53.360	39.428	47.848	1.00	9.62	6	1122	H	PHE A 141	41.672	47.993	47.908	1.00	10.83	7
1070	ATOM	O	ALA A 135	53.052	40.158	48.834	1.00	9.91	8	1123	CA	PHE A 141	40.554	48.858	47.231	1.00	10.94	6
1071	ATOM	H	TRP A 136	52.718	39.492	46.872	1.00	9.28	7	1124	CB	PHE A 141	39.237	47.897	47.618	1.00	8.15	6
1072	ATOM	CA	TRP A 136	51.676	40.473	46.354	1.00	8.76	6	1125	C1	PHE A 141	39.346	46.381	47.561	1.00	6.78	6
1073	ATOM	CB	TRP A 136	51.683	40.690	44.846	1.00	9.45	6	1126	CD1	PHE A 141	39.041	45.816	48.673	1.00	5.88	6
1074	ATOM	C	TRP A 136	52.938	41.438	44.430	1.00	12.78	6	1127	CD2	PHE A 141	39.793	45.725	48.453	1.00	5.72	6
1075	ATOM	C	TRP A 136	53.068	42.081	44.426	1.00	13.09	6	1128	CE1	PHE A 141	39.150	44.223	48.627	1.00	6.27	6
1076	ATOM	CE2	TRP A 136	54.343	43.162	43.888	1.00	14.31	6	1129	CE2	PHE A 141	39.930	44.318	46.407	1.00	5.00	6
1077	ATOM	CE3	TRP A 136	52.234	43.924	44.799	1.00	11.71	6	1130	C1	PHE A 141	39.607	43.584	47.478	1.00	5.00	6
1078	ATOM	CD1	TRP A 136	54.098	40.924	43.934	1.00	13.63	6	1131	C	PHE A 141	40.372	50.134	47.543	1.00	11.05	6
1079	ATOM	HE1	TRP A 136	54.956	41.951	43.599	1.00	15.49	7	1132	O	PHE A 141	39.377	50.553	48.103	1.00	10.80	8
1080	ATOM	C22	TRP A 136	54.866	44.456	43.772	1.00	14.17	6	1133	H	PHE A 142	41.402	50.934	47.254	1.00	11.32	7
1081	ATOM	C23	TRP A 136	52.680	45.213	44.827	1.00	12.36	6	1134	CD	PHE A 142	42.645	50.440	46.634	1.00	11.43	6
1082	ATOM	CH2	TRP A 136	53.971	45.463	44.144	1.00	13.78	6	1135	CA	PHE A 142	41.462	52.386	47.515	1.00	11.27	6
1083	ATOM	C	TRP A 136	50.336	39.995	46.811	1.00	8.40	6	1136	CB	PHE A 142	42.980	52.829	47.190	1.00	11.50	6
1084	ATOM	O	TRP A 136	49.535	39.452	46.066	1.00	8.39	8	1137	CG	PHE A 142	43.300	51.728	46.191	1.00	11.68	6
1085	ATOM	H	TRP A 137	48.844	39.707	48.763	1.00	7.75	6	1138	O	PHE A 142	40.424	53.179	46.766	1.00	11.03	6
1086	ATOM	CG1	TRP A 137	49.275	38.704	49.864	1.00	7.93	6	1139	C	PHE A 142	39.933	54.100	47.431	1.00	11.24	8
1087	ATOM	CG2	TRP A 137	49.351	39.218	50.701	1.00	8.77	8	1140	H	GLY A 143	39.984	52.964	45.545	1.00	10.61	7
1088	ATOM	CG2	TRP A 137	49.647	37.387	49.327	1.00	8.10	6	1141	CA	GLY A 143	38.950	53.703	44.905	1.00	10.26	6
1089	ATOM	C	TRP A 137	48.040	40.772	49.490	1.00	7.59	6	1142	C	GLY A 143	37.544	53.272	45.330	1.00	10.29	6
1090	ATOM	O	TRP A 137	47.063	40.370	50.112	1.00	7.99	8	1143	C	GLY A 143	36.578	54.011	45.134	1.00	10.11	8
1091	ATOM	H	ASP A 138	48.425	42.026	49.486	1.00	7.55	7	1144	H	ARG A 144	37.337	52.102	45.941	1.00	10.41	7
1092	ATOM	CA	ASP A 138	47.680	43.038	50.221	1.00	7.91	6	1145	CA	ARG A 144	36.034	51.630	46.365	1.00	10.66	6
1093	ATOM	CB	ASP A 138	48.667	44.060	50.793	1.00	10.34	6	1146	CB	ARG A 144	35.855	50.122	46.066	1.00	6.45	6
1094	ATOM	CG	ASP A 138	48.054	45.085	51.762	1.00	14.50	6	1147	CG	ARG A 144	34.545	49.572	46.609	1.00	6.10	6
1095	ATOM	CG	ASP A 138	46.820	45.294	51.681	1.00	14.46	6	1148	CD	ARG A 144	34.074	48.222	46.139	1.00	6.59	6
1096	ATOM	CG1	ASP A 138	48.845	45.781	52.416	1.00	16.18	8	1149	HE	ARG A 144	35.003	47.110	46.397	1.00	7.45	7
1097	ATOM	CG2	ASP A 138	46.627	43.671	49.316	1.00	8.01	6	1150	C2	ARG A 144	35.062	46.377	47.500	1.00	7.53	6
1098	ATOM	C	ASP A 138	47.039	44.379	48.405	1.00	7.97	8	1151	WH1	ARG A 144	35.983	45.402	47.826	1.00	8.54	7
1099	ATOM	H	PHE A 139	45.334	43.427	49.520	1.00	8.46	7	1152	WH2	ARG A 144	34.219	46.599	48.511	1.00	6.60	7
1100	ATOM	CA	PHE A 139	44.298	44.016	48.652	1.00	9.00	6	1153	C	ARG A 144	35.736	51.908	47.869	1.00	11.31	4
1101	ATOM	CB	PHE A 139	43.394	43.011	47.964	1.00	7.03	6	1154	O	ARG A 144	34.643	52.176	48.348	1.00	11.03	8
1102	ATOM	CG	PHE A 139	44.078	42.176	46.892	1.00	8.72	6	1155	H	GLY A 145	36.813	51.894	48.658	1.00	11.78	7
1103	ATOM	CG1	PHE A 139	44.948	41.138	47.287	1.00	7.30	6	1156	CA	GLY A 145	36.758	51.954	50.104	1.00	12.35	6
1104	ATOM	CG2	PHE A 139	43.835	42.398	45.538	1.00	7.95	6	1157	C	GLY A 145	35.922	50.757	50.584	1.00	12.97	6
1105	ATOM	C	PHE A 139	45.600	40.359	46.350	1.00	8.64	6	1158	O	GLY A 145	34.169	49.601	50.164	1.00	13.32	8
1106	ATOM	CE1	PHE A 139	44.469	41.605	44.591	1.00	8.85	6	1159	H	ASH A 146	34.906	51.057	51.416	1.00	12.95	7
1107	ATOM	CE2	PHE A 139	45.335	40.593	44.979	1.00	9.11	6	1160	CA	ASH A 146	34.070	49.991	51.970	1.00	12.83	6
1108	ATOM	C	PHE A 139	43.461	44.987	49.487	1.00	9.73	6	1161	CB	ASH A 146	33.889	50.195	51.493	1.00	15.58	6
1109	ATOM	O	PHE A 139	42.707	44.536	50.343	1.00	9.71	8	1162	CG	ASH A 146	35.151	49.936	54.288	1.00	19.40	6
1110	ATOM	H	ARG A 140	43.599	48.294	49.178	1.00	10.52	7	1163	CG1	ASH A 146	34.065	49.159	53.989	1.00	20.79	8
1111	ATOM	CG	ARG A 140	42.823	47.246	49.985	1.00	11.46	6	1164	CG2	ASH A 146	32.684	50.678	55.410	1.00	20.44	7
1112	ATOM	CB	ARG A 140	43.647	48.263	50.745	1.00	17.79	8	1165	C	ASH A 146	32.689	49.855	51.336	1.00	12.13	6
1113	ATOM	C	ARG A 140							1166	O	ASH A 146	31.905	49.168	52.002	1.00	12.08	8

1273	CG	H15 A 157	62.236	36.398	53.732	1.00	5.00	6	1526	CG	H15 A 163	59.639	37.017	39.046	1.00	14.61	6
1274	CG	H15 A 157	41.820	36.018	54.866	1.00	5.00	6	1527	CG	H15 A 163	60.210	38.279	39.139	1.00	16.01	6
1275	CG	H15 A 157	42.426	37.765	53.793	1.00	5.10	7	1528	CG	H15 A 163	57.008	35.969	44.102	1.00	12.82	6
1276	CG	H15 A 157	41.880	38.216	54.935	1.00	6.49	7	1529	CG	H15 A 163	56.235	36.100	45.012	1.00	12.72	6
1277	CG	H15 A 157	41.398	37.147	55.588	1.00	5.12	7	1530	CG	H15 A 163	58.298	38.130	44.243	1.00	13.51	7
1278	CG	H15 A 157	43.696	35.673	51.753	1.00	5.75	6	1531	CG	H15 A 163	58.961	36.679	45.420	1.00	14.00	6
1279	CG	H15 A 157	43.028	33.056	50.978	1.00	5.63	8	1532	CG	H15 A 163	60.073	35.796	45.937	1.00	13.67	6
1280	CG	H15 A 157	45.182	33.311	51.471	1.00	5.60	7	1533	CG	H15 A 163	60.891	36.513	47.003	1.00	14.44	6
1281	CG	H15 A 157	45.722	32.597	50.312	1.00	5.84	8	1534	CG	H15 A 163	60.392	37.464	47.682	1.00	14.16	8
1282	CG	H15 A 157	46.578	33.527	49.412	1.00	5.00	6	1535	CG	H15 A 163	62.070	36.096	47.153	1.00	15.41	8
1283	CG	H15 A 157	45.667	34.764	48.092	1.00	5.00	6	1536	CG	H15 A 163	59.500	38.004	44.913	1.00	14.37	6
1284	CG	H15 A 157	46.099	35.994	49.658	1.00	5.00	6	1537	CG	H15 A 163	60.491	37.969	44.125	1.00	14.14	8
1285	CG	H15 A 157	44.972	34.708	47.942	1.00	5.00	6	1538	CG	H15 A 163	59.024	39.109	45.390	1.00	14.96	7
1286	CG	H15 A 157	45.618	37.147	49.206	1.00	6.00	6	1539	CG	H15 A 163	58.453	41.456	45.466	1.00	15.08	6
1287	CG	H15 A 157	44.300	35.931	47.568	1.00	5.36	8	1540	CG	H15 A 163	58.724	42.887	45.070	1.00	16.95	6
1288	CG	H15 A 157	46.580	37.135	50.692	1.00	5.65	6	1541	CG	H15 A 163	58.627	43.079	43.504	1.00	18.88	6
1289	CG	H15 A 157	47.192	31.311	51.800	1.00	5.98	8	1542	CG	H15 A 163	59.126	44.095	43.075	1.00	22.59	8
1290	CG	H15 A 157	46.638	38.334	49.806	1.00	5.59	7	1543	CG	H15 A 163	58.071	42.288	42.822	1.00	19.30	8
1291	CG	H15 A 157	47.461	29.211	50.022	1.00	5.30	6	1544	CG	H15 A 163	60.843	40.736	45.498	1.00	16.33	6
1292	CG	H15 A 157	46.924	27.979	49.262	1.00	5.00	6	1545	CG	H15 A 163	61.504	41.590	44.951	1.00	16.30	8
1293	CG	H15 A 157	45.876	27.378	50.090	1.00	5.58	6	1546	CG	H15 A 163	61.227	40.104	46.593	1.00	18.71	7
1294	CG	H15 A 157	45.988	27.501	51.360	1.00	6.12	8	1547	CG	H15 A 163	62.499	40.241	47.255	1.00	17.23	6
1295	CG	H15 A 157	44.852	26.813	49.700	1.00	5.00	8	1548	CG	H15 A 163	62.471	39.215	48.415	1.00	17.88	6
1296	CG	H15 A 157	48.876	29.377	49.478	1.00	5.70	6	1549	CG	H15 A 163	63.157	39.838	49.443	1.00	21.31	8
1297	CG	H15 A 157	49.808	28.719	49.999	1.00	6.04	8	1550	CG	H15 A 163	63.694	39.857	46.363	1.00	17.59	6
1298	CG	H15 A 157	49.083	30.164	48.444	1.00	5.67	7	1551	CG	H15 A 163	64.511	40.670	45.931	1.00	17.48	8
1299	CG	H15 A 157	50.472	31.296	46.798	1.00	6.82	6	1552	CG	H15 A 163	65.756	38.534	46.062	1.00	17.53	7
1300	CG	H15 A 157	51.622	31.520	46.724	1.00	6.74	8	1553	CG	H15 A 163	66.754	37.962	45.202	1.00	17.50	6
1301	CG	H15 A 157	51.756	32.488	45.174	1.00	8.08	6	1554	CG	H15 A 163	66.972	36.483	45.538	1.00	18.49	6
1302	CG	H15 A 157	52.023	33.869	45.775	1.00	9.05	6	1555	CG	H15 A 163	65.372	36.319	46.984	1.00	19.67	6
1303	CG	H15 A 157	53.582	31.055	44.591	1.00	8.66	8	1556	CG	H15 A 163	65.413	34.810	47.294	1.00	22.11	6
1304	CG	H15 A 157	53.158	32.846	43.215	1.00	10.00	7	1557	CG	H15 A 163	65.554	34.699	48.736	1.00	24.69	7
1305	CG	H15 A 157	54.278	32.418	42.372	1.00	11.36	6	1558	CG	H15 A 163	66.639	35.047	49.658	1.00	27.34	6
1306	CG	H15 A 157	53.786	32.031	40.983	1.00	15.10	6	1559	CG	H15 A 163	65.027	34.853	50.954	1.00	28.95	7
1307	CG	H15 A 157	53.111	33.242	40.352	1.00	19.35	6	1560	CG	H15 A 163	65.179	37.757	42.880	1.00	17.29	8
1308	CG	H15 A 157	52.930	34.331	40.947	1.00	19.47	8	1561	CG	H15 A 163	63.124	38.406	43.386	1.00	17.25	7
1309	CG	H15 A 157	52.765	32.956	39.169	1.00	22.93	8	1562	CG	H15 A 163	62.636	38.491	42.048	1.00	17.27	6
1310	CG	H15 A 157	53.381	33.455	42.149	1.00	11.95	6	1563	CG	H15 A 163	62.318	39.579	41.203	1.00	20.36	6
1311	CG	H15 A 157	56.107	33.336	41.131	1.00	12.10	8	1564	CG	H15 A 163	62.018	40.920	41.752	1.00	23.95	6
1312	CG	H15 A 157	55.489	34.435	43.048	1.00	12.03	7	1565	CG	H15 A 163	63.805	42.120	41.289	1.00	26.67	6
1313	CG	H15 A 157	56.533	35.418	42.793	1.00	12.54	6	1566	CG	H15 A 163	62.855	43.415	41.686	1.00	28.90	6
1314	CG	H15 A 157	55.954	36.485	41.881	1.00	12.40	6	1567	CG	H15 A 163	62.850	43.694	43.201	1.00	38.66	7
1315	CG	H15 A 157	56.925	37.600	41.631	1.00	13.20	6	1568	CG	H15 A 163	62.786	37.148	43.352	1.00	17.23	8
1316	CG	H15 A 157	58.014	37.602	40.715	1.00	14.18	6	1569	CG	H15 A 163	63.337	37.062	40.229	1.00	17.13	8
1317	CG	H15 A 157	58.646	38.869	40.826	1.00	15.32	6	1570	CG	H15 A 163	62.203	36.106	41.956	1.00	16.95	7
1318	CG	H15 A 157	58.646	38.869	40.826	1.00	15.32	6	1571	CG	H15 A 163	62.199	34.766	41.380	1.00	16.59	6
1319	CG	H15 A 157	58.646	38.869	40.826	1.00	15.32	6	1572	CG	H15 A 163	61.064	33.751	43.115	1.00	17.17	6
1320	CG	H15 A 157	58.646	38.869	40.826	1.00	15.32	6	1573	CG	H15 A 163	64.599	34.139	42.040	1.00	16.91	6
1321	CG	H15 A 157	58.646	38.869	40.826	1.00	15.32	6	1574	CG	H15 A 163	63.641	33.597	43.557	1.00	17.77	6
1322	CG	H15 A 157	58.646	38.869	40.826	1.00	15.32	6	1575	CG	H15 A 163	63.595	32.811	44.434	1.00	18.17	6
1323	CG	H15 A 157	58.646	38.869	40.826	1.00	15.32	6	1576	CG	H15 A 163	63.595	32.811	44.434	1.00	18.17	6
1324	CG	H15 A 157	58.646	38.869	40.826	1.00	15.32	6	1577	CG	H15 A 163	63.595	32.811	44.434	1.00	18.17	6
1325	CG	H15 A 157	58.646	38.869	40.826	1.00	15.32	6	1578	CG	H15 A 163	63.595	32.811	44.434	1.00	18.17	6

1379	C	1LE A 169	60.748	34.265	41.354	1.00	16.43	6	1432	CE1 PHE A 175	50.443	33.823	50.320	1.00	7.64	6
1380	G	1LE A 169	59.894	34.602	42.175	1.00	15.97	8	1433	CE2 PHE A 175	52.585	33.103	49.614	1.00	4.81	6
1381	H	2ER A 170	60.458	33.469	40.342	1.00	16.39	7	1434	CZ PHE A 175	51.517	33.983	49.476	1.00	7.21	6
1382	CA	5ER A 170	59.209	32.808	40.120	1.00	16.32	6	1435	C PHE A 175	52.567	28.942	53.770	1.00	11.49	6
1383	CB	5ER A 170	58.830	32.767	38.442	1.00	16.20	6	1436	D PHE A 175	51.868	27.912	53.875	1.00	11.44	8
1384	CG	5ER A 170	57.519	32.181	38.607	1.00	22.81	8	1437	H ARG A 176	53.286	29.352	54.813	1.00	11.77	7
1385	C	5ER A 170	59.304	31.335	40.518	1.00	16.18	6	1438	CA ARG A 176	51.328	28.725	56.129	1.00	12.20	6
1386	D	5ER A 170	60.106	30.599	39.906	1.00	16.17	8	1439	CG ARG A 176	54.684	28.802	56.775	1.00	13.53	6
1387	H	ARG A 171	58.531	30.882	41.508	1.00	15.84	7	1440	CO ARG A 176	55.788	27.778	58.372	1.00	14.88	6
1388	CA	ARG A 171	58.594	29.492	41.954	1.00	15.28	6	1441	CG ARG A 176	55.188	26.438	58.823	1.00	15.37	6
1389	CB	ARG A 171	59.448	29.168	43.184	1.00	17.32	6	1442	WE ARG A 176	56.133	25.355	56.737	1.00	15.69	7
1390	CG	ARG A 171	60.894	29.497	43.152	1.00	19.88	6	1443	CZ ARG A 176	56.118	24.277	55.962	1.00	16.02	6
1391	CO	ARG A 171	61.825	28.448	42.555	1.00	23.48	6	1444	WH1 ARG A 176	55.150	24.837	55.065	1.00	16.35	7
1392	HE	ARG A 171	63.204	28.981	42.666	1.00	27.05	7	1445	WH2 ARG A 176	57.151	23.430	56.062	1.00	16.02	7
1393	CZ	ARG A 171	63.651	29.577	41.558	1.00	29.43	6	1446	C ARG A 176	52.330	29.528	56.994	1.00	12.82	8
1394	WH1 ARG A 171	62.999	29.718	40.256	1.00	30.87	7	1447	D ARG A 176	52.303	30.774	56.778	1.00	12.92	8	
1395	WH2 ARG A 171	64.884	30.070	41.191	1.00	30.59	7	1448	H GLY A 177	51.540	28.911	57.850	1.00	13.07	7	
1396	C	ARG A 171	57.052	29.164	42.380	1.00	14.63	6	1449	CA GLY A 177	50.590	29.656	58.637	1.00	13.84	6
1397	H	1LE A 172	56.737	27.949	42.824	1.00	13.80	7	1450	C GLY A 177	49.734	28.715	59.449	1.00	14.51	6
1398	CA	1LE A 172	55.389	27.671	43.556	1.00	13.02	6	1451	D GLY A 177	50.056	27.682	59.489	1.00	15.11	8
1399	CB	1LE A 172	54.752	26.357	42.862	1.00	11.93	6	1452	H GLU A 178	48.649	29.125	60.069	1.00	14.47	7
1400	CG	1LE A 172	53.502	26.058	43.656	1.00	11.06	6	1453	CA GLU A 178	47.810	28.232	60.859	1.00	14.86	6
1401	CO	1LE A 172	54.360	26.386	41.554	1.00	11.59	6	1454	CB GLU A 178	46.912	29.831	61.833	1.00	15.74	6
1402	C	1LE A 172	53.920	25.010	40.927	1.00	12.47	6	1455	CB GLU A 178	47.575	29.715	63.000	1.00	16.47	6
1403	HE	1LE A 172	56.218	26.808	45.489	1.00	12.55	8	1456	CO GLU A 178	48.458	28.762	63.819	1.00	18.26	6
1404	C	1LE A 172	55.639	27.730	44.867	1.00	12.55	6	1457	CE1 GLU A 178	48.216	27.504	63.969	1.00	19.50	8
1405	H	1LE A 172	56.218	26.808	45.489	1.00	12.52	8	1458	CE2 GLU A 178	49.408	29.266	64.376	1.00	16.85	8
1406	H	PHE A 173	55.290	28.812	45.529	1.00	11.95	7	1459	C GLU A 178	46.961	27.310	59.957	1.00	15.02	6
1407	CA	PHE A 173	55.444	28.982	46.956	1.00	11.52	6	1460	D GLU A 178	46.138	27.801	59.151	1.00	15.35	8
1408	CB	PHE A 173	55.613	30.424	47.326	1.00	8.83	6	1461	H GLY A 179	47.146	26.015	60.032	1.00	14.81	7
1409	CG	PHE A 173	57.088	30.932	46.719	1.00	8.19	6	1462	CA GLY A 179	46.450	25.842	59.221	1.00	14.68	6
1410	CO	PHE A 173	57.088	30.932	46.719	1.00	8.19	6	1463	C GLY A 179	46.692	25.231	57.702	1.00	14.28	6
1411	CE1 PHE A 173	58.313	30.470	47.211	1.00	8.07	6	1464	D GLY A 179	45.709	24.906	56.979	1.00	14.54	8	
1412	CE2 PHE A 173	58.277	32.307	45.123	1.00	8.69	6	1465	H LYS A 180	47.854	25.708	57.243	1.00	13.43	7	
1413	CZ PHE A 173	59.512	30.949	46.686	1.00	8.72	6	1466	CA LYS A 180	48.022	25.959	55.824	1.00	12.55	6	
1414	D PHE A 173	59.484	31.844	45.607	1.00	7.75	6	1467	CB LYS A 180	49.163	26.955	55.831	1.00	11.68	6	
1415	C	PHE A 173	56.189	28.583	47.688	1.00	11.50	6	1468	CG LYS A 180	48.825	28.409	55.814	1.00	11.89	6
1416	D	PHE A 173	53.189	29.085	47.372	1.00	11.79	8	1469	CO LYS A 180	47.710	26.914	54.938	1.00	9.28	6
1417	H	LYS A 174	54.257	27.696	48.657	1.00	11.28	7	1470	CE LYS A 180	47.355	30.371	55.116	1.00	9.37	6
1418	CA	LYS A 174	53.185	27.303	49.524	1.00	11.02	6	1471	H2 LYS A 180	46.097	30.683	54.339	1.00	9.60	7
1419	CB	LYS A 174	53.268	25.849	49.981	1.00	7.54	6	1472	C LYS A 180	48.271	24.676	55.037	1.00	12.15	6
1420	CG	LYS A 174	52.045	25.443	50.779	1.00	6.03	6	1473	D LYS A 180	49.150	23.919	55.465	1.00	12.30	8
1421	C	LYS A 174	51.880	23.947	50.993	1.00	5.90	6	1474	H ALA A 181	47.571	24.402	53.925	1.00	11.19	7
1422	CE	LYS A 174	53.109	23.439	51.713	1.00	6.00	6	1475	CA ALA A 181	47.120	23.287	51.761	1.00	8.27	6
1423	H2	LYS A 174	52.991	22.034	52.174	1.00	5.20	7	1476	CB ALA A 181	47.183	21.975	53.825	1.00	8.27	6
1424	C	LYS A 174	53.313	28.195	50.767	1.00	11.19	6	1477	C ALA A 181	46.125	23.952	51.862	1.00	8.95	8
1425	D	LYS A 174	54.402	28.117	51.408	1.00	11.32	8	1478	D ALA A 181	47.457	22.762	50.604	1.00	8.84	7
1426	H	PHE A 175	52.357	28.950	51.264	1.00	11.10	7	1479	H LYS A 182	47.457	23.762	50.604	1.00	8.84	7
1427	CA	PHE A 175	52.555	29.759	52.486	1.00	11.23	6	1480	CA LYS A 182	47.232	22.145	48.309	1.00	6.73	6
1428	CB	PHE A 175	51.440	30.864	52.518	1.00	9.58	6	1481	CO LYS A 182	48.674	22.689	47.966	1.00	5.79	6
1429	CG	PHE A 175	51.497	31.920	51.427	1.00	9.11	6	1482	CE LYS A 182	49.003	23.922	47.558	1.00	5.00	6
1430	CO	PHE A 175	50.610	32.806	51.283	1.00	8.73	6	1483	CE2 LYS A 182						
1431	CE1 PHE A 175								1484	CE2 LYS A 182						

ATOM	1485	CE3	TRP	A	182	48.278	25.127	47.341	1.00	5.00	6	6	1538	CA	SER	A	188	45.189	15.208	41.353	1.00	9.72	6	6
ATOM	1486	CD1	TRP	A	182	49.768	21.861	48.002	1.00	5.63	6	6	1539	CB	SER	A	188	44.986	13.770	41.859	1.00	10.83	6	6
ATOM	1487	HE1	TRP	A	182	50.660	22.616	47.616	1.00	5.04	7	7	1540	OG	SER	A	188	44.547	12.983	40.714	1.00	12.11	6	6
ATOM	1488	C22	TRP	A	182	51.110	23.022	46.895	1.00	5.00	6	6	1541	C	SER	A	188	46.315	15.213	40.288	1.00	9.72	6	6
ATOM	1489	C23	TRP	A	182	48.966	26.236	46.927	1.00	5.00	6	6	1542	O	SER	A	188	47.239	14.548	40.729	1.00	9.62	6	6
ATOM	1490	CH2	TRP	A	182	50.376	26.166	46.723	1.00	5.00	6	6	1543	N	GLU	A	189	46.009	15.968	39.192	1.00	9.68	7	7
ATOM	1491	C	TRP	A	182	45.218	22.348	49.787	1.00	8.52	6	6	1544	CA	GLU	A	189	47.091	16.143	38.252	1.00	9.58	6	6
ATOM	1492	O	TRP	A	182	45.029	21.400	50.552	1.00	8.24	6	6	1545	CB	GLU	A	189	46.761	17.025	37.029	1.00	12.65	6	6
ATOM	1493	N	ASP	A	183	44.187	22.939	49.183	1.00	8.61	7	7	1546	CC	GLU	A	189	45.553	16.361	36.202	1.00	14.93	6	6
ATOM	1494	CA	ASP	A	183	42.814	22.566	49.339	1.00	8.57	6	6	1547	CB	GLU	A	189	44.958	17.419	35.359	1.00	16.06	6	6
ATOM	1495	CB	ASP	A	183	41.746	23.407	48.669	1.00	7.64	6	6	1548	OE1	GLU	A	189	44.060	18.118	35.868	1.00	16.06	6	6
ATOM	1496	CC	ASP	A	183	41.829	24.866	49.207	1.00	7.97	6	6	1549	OE2	GLU	A	189	45.364	17.496	34.187	1.00	19.90	6	6
ATOM	1497	OO1	ASP	A	183	42.136	25.011	50.384	1.00	5.19	8	8	1550	C	GLU	A	189	48.208	16.888	38.998	1.00	9.38	6	6
ATOM	1498	OO2	ASP	A	183	41.604	25.903	48.623	1.00	7.20	8	8	1551	O	GLU	A	189	47.948	17.852	39.783	1.00	9.35	6	6
ATOM	1499	C	ASP	A	183	42.678	21.163	48.661	1.00	8.68	6	6	1552	N	ASP	A	190	49.447	16.512	38.785	1.00	9.02	7	7
ATOM	1500	O	ASP	A	183	43.392	20.764	47.757	1.00	8.29	8	8	1553	CA	ASP	A	190	50.591	17.137	39.437	1.00	8.98	6	6
ATOM	1501	N	TRP	A	184	41.655	20.526	49.221	1.00	8.85	7	7	1554	CB	ASP	A	190	50.708	18.629	39.139	1.00	11.63	6	6
ATOM	1502	CA	TRP	A	184	41.337	19.214	48.816	1.00	9.31	6	6	1555	CC	ASP	A	190	50.842	19.067	37.714	1.00	13.22	6	6
ATOM	1503	CB	TRP	A	184	42.068	18.015	49.485	1.00	9.16	6	6	1556	OO1	ASP	A	190	51.353	18.489	36.913	1.00	13.96	6	6
ATOM	1504	CC	TRP	A	184	41.858	16.719	48.616	1.00	9.24	6	6	1557	OO2	ASP	A	190	50.145	20.093	37.234	1.00	14.84	7	7
ATOM	1505	CD2	TRP	A	184	42.591	16.211	47.580	1.00	9.64	6	6	1558	C	ASP	A	190	50.548	16.928	40.959	1.00	8.84	6	6
ATOM	1506	CE2	TRP	A	184	41.670	14.896	47.384	1.00	9.60	6	6	1559	O	ASP	A	190	51.020	17.773	41.750	1.00	9.06	6	6
ATOM	1507	CE3	TRP	A	184	43.240	16.730	46.596	1.00	8.61	6	6	1560	N	GLY	A	191	49.949	15.856	41.439	1.00	8.36	7	7
ATOM	1508	CO1	TRP	A	184	41.009	15.713	49.308	1.00	10.78	6	6	1561	CA	GLY	A	191	49.772	15.467	42.809	1.00	7.95	6	6
ATOM	1509	HE1	TRP	A	184	41.019	16.828	48.426	1.00	9.86	7	7	1562	C	GLY	A	191	48.597	16.148	43.430	1.00	7.74	6	6
ATOM	1510	C22	TRP	A	184	42.149	14.151	46.250	1.00	9.85	6	6	1563	O	GLY	A	191	47.747	15.586	44.065	1.00	7.89	6	6
ATOM	1511	C23	TRP	A	184	43.547	15.968	45.479	1.00	9.71	6	6	1564	N	ASP	A	192	48.537	17.450	43.284	1.00	7.66	7	7
ATOM	1512	CH2	TRP	A	184	43.008	16.693	45.316	1.00	9.96	6	6	1565	CA	ASP	A	192	47.472	18.353	43.732	1.00	7.21	6	6
ATOM	1513	C	TRP	A	184	39.766	18.960	48.936	1.00	9.70	6	6	1566	CB	ASP	A	192	47.596	18.649	45.227	1.00	8.14	6	6
ATOM	1514	O	TRP	A	184	39.093	19.322	49.789	1.00	10.01	8	8	1567	CC	ASP	A	192	46.628	19.665	45.785	1.00	7.93	6	6
ATOM	1515	N	GLU	A	185	39.594	18.432	47.785	1.00	9.88	7	7	1568	OO1	ASP	A	192	46.584	20.794	45.287	1.00	8.55	8	8
ATOM	1516	CA	GLU	A	185	39.263	17.724	46.655	1.00	9.32	6	6	1569	OO2	ASP	A	192	45.839	19.388	46.805	1.00	7.17	7	7
ATOM	1517	CB	GLU	A	185	38.801	16.787	46.321	1.00	11.19	6	6	1570	C	ASP	A	192	47.572	19.615	42.863	1.00	6.90	6	6
ATOM	1518	CC	GLU	A	185	38.829	15.981	45.132	1.00	11.41	6	6	1571	O	ASP	A	193	46.574	20.328	42.910	1.00	6.69	8	8
ATOM	1519	CD	GLU	A	185	38.070	14.631	44.816	1.00	13.77	6	6	1572	N	TRP	A	193	46.517	19.881	42.099	1.00	6.77	7	7
ATOM	1520	CE1	GLU	A	185	37.347	14.228	45.559	1.00	14.04	8	8	1573	CA	TRP	A	193	46.405	20.986	41.210	1.00	7.00	6	6
ATOM	1521	CE2	GLU	A	185	38.349	14.001	43.768	1.00	14.41	8	8	1574	CB	TRP	A	193	45.725	20.535	39.867	1.00	7.52	6	6
ATOM	1522	C	GLU	A	185	39.394	18.759	45.479	1.00	8.78	6	6	1575	CC	TRP	A	193	46.348	21.143	38.659	1.00	8.30	6	6
ATOM	1523	O	GLU	A	185	38.591	19.636	45.204	1.00	8.92	8	8	1576	CB1	TRP	A	193	46.218	20.596	37.585	1.00	8.97	6	6
ATOM	1524	N	VAL	A	186	40.502	18.566	44.792	1.00	8.34	7	7	1577	CE1	TRP	A	193	46.841	21.202	36.283	1.00	9.17	6	6
ATOM	1525	CA	VAL	A	186	40.610	19.386	43.583	1.00	8.33	6	6	1578	CE2	TRP	A	193	47.096	23.301	38.738	1.00	8.68	6	6
ATOM	1526	CB	VAL	A	186	41.887	20.506	43.735	1.00	8.32	6	6	1579	CE3	TRP	A	193	47.695	22.928	37.673	1.00	9.08	6	6
ATOM	1527	CO1	VAL	A	186	41.196	21.617	44.616	1.00	7.05	6	6	1580	CE2	TRP	A	193	47.564	22.343	36.424	1.00	9.39	6	6
ATOM	1528	CO2	VAL	A	186	43.173	20.110	44.308	1.00	5.20	6	6	1581	OH	TRP	A	193	45.846	22.201	41.776	1.00	9.62	6	6
ATOM	1529	C	VAL	A	186	41.364	18.291	42.578	1.00	8.42	6	6	1582	C	TRP	A	193	45.034	22.979	41.061	1.00	6.78	8	8
ATOM	1530	O	VAL	A	186	41.505	17.111	42.956	1.00	8.25	8	8	1583	O	TRP	A	193	45.662	22.448	43.866	1.00	6.98	7	7
ATOM	1531	N	SER	A	187	41.735	18.666	41.367	1.00	8.40	7	7	1584	N	ASP	A	194	45.102	23.587	43.773	1.00	6.81	6	6
ATOM	1532	CA	SER	A	187	42.313	17.723	39.445	1.00	8.96	6	6	1585	CA	ASP	A	194	45.338	23.579	45.279	1.00	7.26	6	6
ATOM	1533	CB	SER	A	187	42.664	18.432	39.113	1.00	8.95	6	6	1586	CB	ASP	A	194	44.586	24.609	46.082	1.00	8.65	6	6
ATOM	1534	CC	SER	A	187	43.472	17.537	38.328	1.00	8.65	8	8	1587	CC	ASP	A	194	43.590	25.127	45.523	1.00	9.18	8	8
ATOM	1535	C	SER	A	187	43.603	17.153	41.060	1.00	9.46	6	6	1588	OO1	ASP	A	194	44.730	24.922	47.280	1.00	8.87	8	8
ATOM	1536	O	SER	A	187	44.375	17.887	41.684	1.00	9.28	8	8	1589	OO2	ASP	A	194	45.815	24.809	43.156	1.00	6.83	6	6
ATOM	1537	N	SER	A	188	43.908	15.846	40.623	1.00	9.77	7	7	1590	C	ASP	A	194							

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1697	W	ASP A 207	1.00	6.12	7	1750	CA	LVS A 216	28.061	36.774	50.337	1.00	7.39	6
1698	CA	ASP A 207	1.00	6.05	6	1751	CA	LVS A 216	28.618	37.530	51.539	1.00	11.90	6
1699	CB	ASP A 207	1.00	6.37	6	1752	CB	LVS A 216	28.423	39.011	51.741	1.00	17.64	6
1700	CG	ASP A 207	1.00	6.87	6	1753	CG	LVS A 216	29.354	39.548	52.915	1.00	22.01	6
1701	CH	ASP A 207	1.00	7.93	6	1754	CH	LVS A 216	29.770	41.017	52.697	1.00	24.62	6
1702	CI	ASP A 207	1.00	7.93	6	1755	CI	LVS A 216	31.138	41.472	53.171	1.00	24.85	7
1703	CJ	ASP A 207	1.00	6.17	6	1756	CJ	LVS A 216	28.290	37.533	49.821	1.00	7.87	6
1704	Q	ASP A 207	1.00	5.78	6	1757	Q	LVS A 216	27.317	38.174	48.561	1.00	7.02	6
1705	W	VAL A 208	1.00	6.47	7	1758	W	18P A 215	29.481	37.582	48.430	1.00	6.68	7
1706	CA	VAL A 208	1.00	6.58	6	1759	CA	18P A 215	29.726	38.173	47.140	1.00	6.58	6
1707	CB	VAL A 208	1.00	7.47	6	1760	CB	18P A 215	31.216	38.139	46.715	1.00	5.00	6
1708	CC	VAL A 208	1.00	7.06	6	1761	CC	18P A 215	31.353	38.622	45.281	1.00	5.00	6
1709	CD	VAL A 208	1.00	6.71	6	1762	CD	18P A 215	31.418	37.741	44.122	1.00	5.00	6
1710	C	VAL A 208	1.00	6.90	6	1763	CE	18P A 215	31.427	38.564	43.803	1.00	5.00	6
1711	Q	VAL A 208	1.00	6.95	6	1764	CE	18P A 215	31.455	36.349	43.980	1.00	5.00	6
1712	W	VAL A 209	1.00	7.00	6	1765	CE	18P A 215	31.418	39.874	43.430	1.00	5.00	7
1713	CA	VAL A 209	1.00	5.34	6	1766	CE	18P A 215	31.507	38.908	41.720	1.00	5.18	6
1714	CB	VAL A 209	1.00	5.00	6	1767	CE	18P A 215	31.494	35.789	42.707	1.00	5.00	6
1715	CC	VAL A 209	1.00	5.00	6	1768	CE	18P A 215	31.534	36.649	41.559	1.00	5.00	6
1716	CD	VAL A 209	1.00	7.32	6	1769	CE	18P A 215	28.222	38.231	45.223	1.00	6.73	6
1717	C	VAL A 209	1.00	7.32	6	1770	C	GLY A 216	28.716	36.209	46.000	1.00	7.00	7
1718	W	ALA A 210	1.00	7.34	7	1771	C	GLY A 216	26.482	35.990	44.999	1.00	7.12	6
1719	CA	ALA A 210	1.00	7.52	6	1772	W	GLY A 216	27.936	35.541	45.004	1.00	7.24	6
1720	CB	ALA A 210	1.00	7.52	6	1773	CA	GLY A 216	25.868	36.132	43.918	1.00	6.99	8
1721	CC	ALA A 210	1.00	7.58	6	1774	C	GLY A 216	25.955	36.136	46.205	1.00	7.41	7
1722	C	ALA A 210	1.00	7.58	6	1775	Q	GLY A 216	24.531	36.346	46.325	1.00	7.50	6
1723	W	GLU A 211	1.00	7.67	7	1776	W	GLY A 217	24.011	36.340	47.777	1.00	8.38	6
1724	CA	GLU A 211	1.00	9.06	6	1777	CA	GLY A 217	22.627	36.981	48.057	1.00	6.66	6
1725	CB	GLU A 211	1.00	13.89	6	1778	CB	GLY A 217	23.923	34.851	48.131	1.00	7.56	6
1726	CC	GLU A 211	1.00	16.28	6	1779	CC	GLY A 217	24.065	34.683	49.629	1.00	7.44	6
1727	CD	GLU A 211	1.00	13.34	6	1780	CD	GLY A 217	24.406	37.971	45.846	1.00	7.47	6
1728	C	GLU A 211	1.00	7.61	6	1781	C	GLY A 217	23.541	38.358	45.092	1.00	7.49	6
1729	W	GLU A 211	1.00	7.56	6	1782	W	GLY A 217	25.329	38.864	46.232	1.00	7.72	7
1730	CA	GLU A 211	1.00	7.56	6	1783	Q	GLY A 217	25.354	40.252	45.814	1.00	7.84	6
1731	C	GLU A 211	1.00	7.56	6	1784	W	GLY A 217	26.556	40.953	46.464	1.00	7.78	6
1732	Q	GLU A 211	1.00	7.56	6	1785	CA	GLY A 218	26.778	43.365	45.975	1.00	8.77	6
1733	W	GLU A 212	1.00	7.17	7	1786	CB	GLY A 218	27.466	44.221	44.817	1.00	9.24	6
1734	CA	GLU A 212	1.00	8.17	6	1787	CC	GLY A 218	28.514	42.168	44.041	1.00	7.35	6
1735	CB	GLU A 212	1.00	9.40	6	1788	CD	GLY A 218	28.112	43.673	46.439	1.00	9.49	6
1736	CC	GLU A 212	1.00	6.87	6	1789	CE	GLY A 218	28.169	45.022	43.903	1.00	9.30	7
1737	CD	GLU A 212	1.00	6.87	6	1790	CE	GLY A 218	29.215	42.962	43.149	1.00	7.92	6
1738	C	GLU A 212	1.00	7.14	6	1791	CE	GLY A 218	29.058	44.371	43.069	1.00	8.47	6
1739	Q	GLU A 212	1.00	6.89	6	1792	CE	GLY A 218	25.395	40.538	44.301	1.00	7.81	6
1740	W	GLU A 213	1.00	9.86	6	1793	CE	GLY A 218	24.708	41.250	43.686	1.00	7.56	8
1741	CA	GLU A 213	1.00	9.86	6	1794	CE	GLY A 218	26.309	39.722	43.653	1.00	8.18	7
1742	CB	GLU A 213	1.00	10.33	6	1795	CE	GLY A 218	26.537	39.789	42.203	1.00	8.37	6
1743	CC	GLU A 213	1.00	7.15	6	1796	CE	GLY A 218	27.703	38.789	41.955	1.00	8.61	6
1744	CD	GLU A 213	1.00	6.94	6	1797	CE	GLY A 218	28.243	38.670	40.554	1.00	9.11	6
1745	C	GLU A 213	1.00	7.01	7	1798	CE	GLY A 218	28.615	39.784	39.810	1.00	9.59	6

1803	CE1	YR	A	219	29.180	39.619	38.541	1.00	9.96	6	ATOM	1856	CB	ASP	A	226	19.357	33.821	34.254	1.00	7.73	6
1804	CE2	YR	A	219	28.416	37.404	40.008	1.00	9.35	6	ATOM	1857	CB	ASP	A	226	18.559	35.071	33.990	1.00	7.95	6
1805	CE2	YR	A	219	28.959	37.265	38.740	1.00	9.78	6	ATOM	1858	CG	ASP	A	226	17.512	35.272	34.681	1.00	10.67	8
1806	CE2	YR	A	219	29.346	38.161	38.821	1.00	10.19	6	ATOM	1859	CG	ASP	A	226	18.962	35.869	33.172	1.00	7.61	8
1807	CE1	YR	A	219	29.899	38.187	36.757	1.00	11.08	8	ATOM	1860	C	ASP	A	226	20.796	32.868	35.806	1.00	7.95	6
1808	C	YR	A	219	25.279	39.259	41.447	1.00	8.69	6	ATOM	1861	C	ASP	A	226	20.213	31.578	35.837	1.00	8.41	8
1809	C	YR	A	219	24.836	39.944	40.527	1.00	8.37	8	ATOM	1862	H	GLY	A	227	22.107	32.836	35.852	1.00	7.65	7
1810	H	ALA	A	220	24.676	38.131	41.869	1.00	9.13	7	ATOM	1863	CA	GLY	A	227	22.992	31.679	35.946	1.00	7.46	6
1811	CA	ALA	A	220	23.427	37.644	41.267	1.00	9.77	6	ATOM	1864	C	GLY	A	227	24.671	32.049	35.990	1.00	7.30	6
1812	CB	ALA	A	220	22.899	36.384	41.881	1.00	8.61	6	ATOM	1865	O	GLY	A	227	24.880	33.197	36.042	1.00	6.95	8
1813	C	ALA	A	220	22.315	38.685	41.371	1.00	10.07	6	ATOM	1866	H	PHE	A	228	25.294	30.990	36.029	1.00	7.33	7
1814	O	ALA	A	220	21.536	38.887	40.377	1.00	10.05	8	ATOM	1867	CA	PHE	A	228	26.742	31.170	36.166	1.00	7.35	6
1815	H	ASN	A	221	22.192	39.338	42.473	1.00	10.39	7	ATOM	1868	CB	PHE	A	228	27.220	30.898	37.558	1.00	6.74	6
1816	CA	ASN	A	221	21.200	60.374	42.757	1.00	11.66	6	ATOM	1869	CG	PHE	A	228	26.640	31.708	38.672	1.00	9.48	6
1817	CB	ASN	A	221	21.013	60.698	44.262	1.00	13.90	6	ATOM	1870	CG	PHE	A	228	25.930	31.082	39.700	1.00	9.82	6
1818	CG	ASN	A	221	20.192	39.543	44.855	1.00	18.18	8	ATOM	1871	CG	PHE	A	228	26.800	33.097	38.702	1.00	8.78	6
1819	CG	ASN	A	221	19.371	38.852	44.227	1.00	19.44	8	ATOM	1872	CE1	PHE	A	228	25.415	31.869	40.731	1.00	10.75	6
1820	CG	ASN	A	221	20.481	39.263	44.125	1.00	19.84	7	ATOM	1873	CE2	PHE	A	228	26.277	33.860	39.746	1.00	9.42	6
1821	C	ASN	A	221	21.524	41.717	42.136	1.00	10.51	6	ATOM	1874	CZ	PHE	A	228	25.590	33.241	40.786	1.00	9.84	6
1822	O	ASN	A	221	20.592	42.323	41.626	1.00	10.40	8	ATOM	1875	C	PHE	A	228	27.245	29.086	36.995	1.00	7.29	6
1823	H	GLU	A	222	22.794	42.125	43.143	1.00	10.51	7	ATOM	1876	O	PHE	A	228	28.791	30.675	34.978	1.00	6.86	7
1824	CA	GLU	A	222	21.160	43.432	41.552	1.00	10.18	6	ATOM	1877	H	ARG	A	229	29.818	29.927	34.305	1.00	6.75	6
1825	CB	GLU	A	222	24.621	43.807	41.791	1.00	11.08	6	ATOM	1878	CA	ARG	A	229	30.172	30.439	32.885	1.00	6.68	6
1826	CG	GLU	A	222	25.013	45.244	41.468	1.00	12.96	6	ATOM	1879	CG	ARG	A	229	31.309	29.551	32.327	1.00	5.59	6
1827	CG	GLU	A	222	24.412	46.283	42.496	1.00	15.13	6	ATOM	1880	CG	ARG	A	229	32.646	30.263	32.584	1.00	7.41	6
1828	CG	GLU	A	222	23.947	45.777	43.576	1.00	15.79	8	ATOM	1881	CG	ARG	A	229	33.701	29.623	31.828	1.00	7.61	7
1829	CG	GLU	A	222	24.381	47.432	42.254	1.00	16.17	8	ATOM	1882	HE	ARG	A	229	34.985	29.905	31.872	1.00	8.29	6
1830	CG	GLU	A	222	22.903	43.428	40.052	1.00	9.82	6	ATOM	1883	CG	ARG	A	229	35.833	29.189	31.139	1.00	7.90	7
1831	O	GLU	A	222	23.470	46.444	39.507	1.00	9.72	8	ATOM	1884	HN1	ARG	A	229	33.388	30.913	32.626	1.00	7.66	7
1832	H	LEU	A	223	23.227	42.343	39.348	1.00	9.48	7	ATOM	1885	HN2	ARG	A	229	30.998	29.916	35.323	1.00	6.49	6
1833	CA	LEU	A	223	23.009	42.319	37.909	1.00	9.43	6	ATOM	1886	C	ARG	A	229	31.518	30.980	35.697	1.00	6.39	8
1834	CB	LEU	A	223	24.300	41.715	37.281	1.00	7.13	6	ATOM	1887	O	ARG	A	229	32.530	28.667	36.752	1.00	5.82	6
1835	CG	LEU	A	223	25.795	42.503	37.478	1.00	5.72	6	ATOM	1888	H	ILE	A	230	33.427	28.711	35.760	1.00	6.19	7
1836	CG	LEU	A	223	26.752	41.715	36.835	1.00	5.00	6	ATOM	1889	CA	ILE	A	230	32.534	27.325	38.616	1.00	5.00	6
1837	CG	LEU	A	223	25.470	43.888	36.880	1.00	5.20	6	ATOM	1890	CB	ILE	A	230	32.219	27.598	37.860	1.00	6.87	6
1838	C	LEU	A	223	21.794	41.558	37.456	1.00	9.44	6	ATOM	1891	CG	ILE	A	230	33.534	27.325	38.616	1.00	5.00	6
1839	O	LEU	A	223	21.561	41.335	36.280	1.00	9.57	8	ATOM	1892	CG	ILE	A	230	31.001	28.126	38.617	1.00	6.60	6
1840	H	SER	A	224	20.993	40.998	38.286	1.00	9.74	7	ATOM	1893	CG	ILE	A	230	30.470	27.073	39.604	1.00	11.75	6
1841	CA	SER	A	224	18.660	40.832	37.156	1.00	10.06	6	ATOM	1894	C	ILE	A	230	33.907	28.409	36.148	1.00	5.56	6
1842	CB	SER	A	224	18.251	41.991	37.901	1.00	19.93	8	ATOM	1895	O	ILE	A	230	34.235	27.368	35.555	1.00	5.42	7
1843	CG	SER	A	224	20.293	38.979	37.047	1.00	9.76	8	ATOM	1896	H	ASP	A	231	34.758	29.428	36.266	1.00	5.02	6
1844	O	SER	A	224	19.648	38.752	36.006	1.00	9.74	8	ATOM	1897	CA	ASP	A	231	36.086	29.323	35.714	1.00	5.00	6
1845	C	SER	A	224	20.293	38.979	37.047	1.00	9.76	8	ATOM	1898	CB	ASP	A	231	36.693	30.746	35.684	1.00	5.00	6
1846	H	LEU	A	225	21.360	38.248	37.445	1.00	9.20	7	ATOM	1899	CG	ASP	A	231	38.078	30.857	35.062	1.00	5.00	6
1847	CA	LEU	A	225	21.770	37.113	36.651	1.00	8.94	6	ATOM	1900	CG	ASP	A	231	38.156	30.984	33.864	1.00	5.00	8
1848	CB	LEU	A	225	23.164	36.688	37.088	1.00	10.36	6	ATOM	1901	CG	ASP	A	231	39.013	31.237	35.828	1.00	5.00	8
1849	CG	LEU	A	225	24.297	37.738	36.958	1.00	11.62	6	ATOM	1902	C	ASP	A	231	37.016	28.427	36.518	1.00	5.00	8
1850	CG	LEU	A	225	25.552	37.169	37.597	1.00	10.68	6	ATOM	1903	O	ASP	A	231	36.987	28.462	37.750	1.00	5.00	8
1851	CG	LEU	A	225	24.524	38.163	35.508	1.00	10.53	6	ATOM	1904	H	ALA	A	232	37.861	27.861	35.619	1.00	5.00	7
1852	C	LEU	A	225	20.793	35.945	36.827	1.00	8.77	6	ATOM	1905	CA	ALA	A	232	38.889	26.846	36.430	1.00	5.00	6
1853	O	LEU	A	225	20.094	35.765	37.796	1.00	8.44	8	ATOM	1906	CB	ALA	A	232	39.930	27.869	36.945	1.00	6.65	6
1854	H	ASP	A	226	20.734	35.084	35.804	1.00	8.55	7	ATOM	1907	C	ALA	A	232	38.515	25.954	37.593	1.00	5.00	6
1855	CA	ASP	A	226	19.950	33.911	35.674	1.00	7.98	6	ATOM	1908	O	ALA	A	232	39.189	25.916	38.626	1.00	5.00	8

A10M	1909	H	ALA A 233	37.399	29.223	37.416	1.00	5.80	7	A10M	1962	CA	SER A 239	32.766	20.656	48.065	1.00	7.57	6
A10M	1910	CA	ALA A 233	36.848	24.420	38.465	1.00	5.45	6	A10M	1963	CB	SER A 239	32.940	19.984	49.417	1.00	7.79	6
A10M	1911	CB	ALA A 233	35.529	23.866	37.899	1.00	6.05	6	A10M	1964	OC	SER A 239	34.169	20.443	49.919	1.00	10.61	8
A10M	1912	C	ALA A 233	35.259	23.310	38.952	1.00	6.80	6	A10M	1965	C	SER A 239	32.410	22.159	48.249	1.00	7.33	6
A10M	1913	O	ALA A 233	37.565	22.943	40.144	1.00	6.16	8	A10M	1966	O	SER A 239	31.237	22.448	48.454	1.00	7.20	8
A10M	1914	K	LVS A 234	38.683	22.764	38.169	1.00	5.81	7	A10M	1967	H	PHE A 240	33.388	23.666	48.168	1.00	7.19	7
A10M	1915	CA	LVS A 234	39.508	21.670	38.618	1.00	6.08	6	A10M	1968	CA	PHE A 240	33.073	24.471	48.275	1.00	7.28	6
A10M	1916	CB	LVS A 234	40.171	20.929	37.485	1.00	5.76	6	A10M	1969	CB	PHE A 240	34.332	25.325	48.382	1.00	7.42	6
A10M	1917	CG	LVS A 234	41.275	21.620	36.794	1.00	6.41	6	A10M	1970	CG	PHE A 240	34.049	26.801	48.123	1.00	7.00	6
A10M	1918	CE	LVS A 234	41.843	20.613	35.671	1.00	7.10	6	A10M	1971	CO1	PHE A 240	33.390	27.560	49.085	1.00	6.31	6
A10M	1919	CE	LVS A 234	43.118	21.208	34.994	1.00	5.42	6	A10M	1972	CO2	PHE A 240	34.413	27.352	48.911	1.00	6.51	6
A10M	1920	HZ	LVS A 234	43.541	20.287	33.901	1.00	5.00	7	A10M	1973	CE1	PHE A 240	33.091	28.886	48.775	1.00	7.11	6
A10M	1921	C	LVS A 234	40.530	22.145	39.648	1.00	6.60	6	A10M	1974	CE2	PHE A 240	34.116	28.674	46.615	1.00	5.97	6
A10M	1922	O	LVS A 234	41.110	21.289	40.336	1.00	6.53	8	A10M	1975	C2	PHE A 240	33.479	29.440	47.555	1.00	5.18	6
A10M	1923	H	HIS A 235	40.709	23.486	39.781	1.00	6.73	7	A10M	1976	C	PHE A 240	32.250	24.980	47.044	1.00	7.54	6
A10M	1924	CA	HIS A 235	41.640	23.999	40.796	1.00	6.75	6	A10M	1977	O	PHE A 240	31.251	25.631	47.191	1.00	7.63	8
A10M	1925	CB	HIS A 235	42.497	23.195	40.296	1.00	6.58	6	A10M	1978	H	LEU A 241	32.639	24.464	49.1838	1.00	7.46	7
A10M	1926	CG	HIS A 235	43.030	24.789	38.959	1.00	6.14	6	A10M	1979	CA	LEU A 241	31.880	24.877	44.661	1.00	7.91	6
A10M	1927	CE	HIS A 235	42.575	25.085	37.724	1.00	7.29	6	A10M	1980	CB	LEU A 241	32.528	24.553	43.318	1.00	5.00	6
A10M	1928	H01	HIS A 235	44.084	23.935	38.789	1.00	5.80	7	A10M	1981	CG	LEU A 241	33.814	25.279	42.944	1.00	5.00	6
A10M	1929	CE1	HIS A 235	44.290	23.756	37.502	1.00	7.11	6	A10M	1982	CO1	LEU A 241	34.520	24.613	41.753	1.00	5.00	6
A10M	1930	HE2	HIS A 235	43.388	24.446	36.829	1.00	6.22	7	A10M	1983	CO2	LEU A 241	33.548	26.754	42.654	1.00	5.00	6
A10M	1931	C	HIS A 235	40.857	26.459	42.002	1.00	6.76	6	A10M	1984	C	LEU A 241	30.418	24.377	44.730	1.00	8.46	6
A10M	1932	O	HIS A 235	41.512	25.942	42.816	1.00	6.54	8	A10M	1985	O	LEU A 241	29.483	29.127	44.303	1.00	0.58	8
A10M	1933	N	ILE A 236	39.583	24.341	42.255	1.00	6.87	7	A10M	1986	H	ARG A 242	30.184	23.774	45.219	1.00	8.61	7
A10M	1934	CA	ILE A 236	38.916	24.866	43.434	1.00	6.87	6	A10M	1987	CA	ARG A 242	28.777	23.774	45.265	1.00	8.61	7
A10M	1935	CB	ILE A 236	37.858	25.949	43.026	1.00	5.00	6	A10M	1988	CB	ARG A 242	28.716	23.286	45.431	1.00	10.58	8
A10M	1936	CE2	ILE A 236	37.089	26.450	44.213	1.00	5.00	6	A10M	1989	CG	ARG A 242	28.819	20.546	46.608	1.00	12.57	6
A10M	1937	CE1	ILE A 236	38.558	27.103	42.238	1.00	5.00	6	A10M	1990	CG	ARG A 242	27.687	19.642	47.094	1.00	13.52	6
A10M	1938	ED1	ILE A 236	37.601	27.999	41.485	1.00	5.00	6	A10M	1991	WE	ARG A 242	28.192	19.659	48.476	1.00	15.26	7
A10M	1939	C	ILE A 236	38.228	28.724	44.193	1.00	7.20	6	A10M	1992	C2	ARG A 242	28.955	18.913	49.256	1.00	17.48	6
A10M	1940	O	ILE A 236	37.587	22.852	43.555	1.00	7.08	8	A10M	1993	H01	ARG A 242	29.464	17.761	48.866	1.00	19.52	7
A10M	1941	N	LVS A 237	38.407	23.693	45.498	1.00	7.57	7	A10M	1994	H02	ARG A 242	29.303	19.263	50.505	1.00	18.04	7
A10M	1942	CA	LVS A 237	37.831	22.688	46.424	1.00	7.74	6	A10M	1995	C	ARG A 242	28.042	23.548	46.379	1.00	8.91	6
A10M	1943	CB	LVS A 237	37.828	23.257	47.866	1.00	9.45	6	A10M	1996	O	ARG A 242	26.891	23.909	46.129	1.00	6.59	8
A10M	1944	CG	LVS A 237	37.355	22.233	48.831	1.00	12.16	6	A10M	1997	H	ASP A 243	26.653	23.828	47.526	1.00	9.00	7
A10M	1945	CE	LVS A 237	37.037	22.463	50.263	1.00	15.99	6	A10M	1998	CA	ASP A 243	27.964	24.591	48.533	1.00	9.47	6
A10M	1946	CE	LVS A 237	37.992	23.114	51.189	1.00	19.56	6	A10M	1999	CB	ASP A 243	28.812	24.581	49.811	1.00	11.98	6
A10M	1947	HZ	LVS A 237	37.579	22.767	52.823	1.00	22.41	7	A10M	2000	CG	ASP A 243	28.766	23.183	50.417	1.00	15.20	6
A10M	1948	C	LVS A 237	36.425	22.314	45.956	1.00	7.39	6	A10M	2001	CO1	ASP A 243	29.580	22.982	51.372	1.00	19.21	8
A10M	1949	O	LVS A 237	35.561	21.187	45.869	1.00	6.92	8	A10M	2002	CO2	ASP A 243	28.049	22.351	50.036	1.00	13.33	8
A10M	1950	H	PHE A 238	36.210	21.082	45.551	1.00	7.45	7	A10M	2003	C	ASP A 243	27.798	26.849	48.117	1.00	9.53	6
A10M	1951	CA	PHE A 238	34.912	20.489	44.946	1.00	7.67	6	A10M	2004	O	ASP A 243	26.797	26.664	48.539	1.00	9.54	8
A10M	1952	CB	PHE A 238	34.921	19.232	44.425	1.00	9.75	6	A10M	2005	H	TRP A 244	28.755	26.581	47.303	1.00	9.34	7
A10M	1953	CB	PHE A 238	35.992	18.884	43.442	1.00	9.75	6	A10M	2006	CA	TRP A 244	28.622	28.005	48.908	1.00	9.20	6
A10M	1954	CO1	PHE A 238	36.888	19.851	42.716	1.00	9.45	6	A10M	2007	CB	TRP A 244	29.862	28.511	46.195	1.00	7.34	6
A10M	1955	CE1	PHE A 238	36.262	17.559	43.199	1.00	9.12	6	A10M	2008	CG	TRP A 244	29.831	29.924	45.719	1.00	8.91	6
A10M	1956	CE2	PHE A 238	37.638	19.448	41.787	1.00	8.83	6	A10M	2009	CO2	TRP A 244	29.442	30.367	44.411	1.00	10.54	6
A10M	1957	CE2	PHE A 238	37.220	17.125	42.292	1.00	8.83	6	A10M	2010	CE2	TRP A 244	29.589	31.773	44.384	1.00	10.38	6
A10M	1958	C2	PHE A 238	37.682	18.097	41.562	1.00	9.31	6	A10M	2011	CE3	TRP A 244	29.020	29.698	43.243	1.00	9.07	6
A10M	1959	C	PHE A 238	33.694	20.870	45.841	1.00	7.61	6	A10M	2012	CE3	TRP A 244	30.168	31.065	46.419	1.00	9.59	7
A10M	1960	O	PHE A 238	32.666	21.356	45.350	1.00	7.47	6	A10M	2013	HE1	TRP A 244	30.036	32.191	45.638	1.00	9.59	7
A10M	1961	H	SER A 239	33.801	20.475	47.113	1.00	7.50	7	A10M	2014	C22	TRP A 244	29.289	32.524	43.219	1.00	9.81	6

2121	CA	YHR	A	258	25.392	26.609	36.450	1.00	8.71	6	AT04	2174	H	GLN	A	264	39.758	18.950	31.301	1.00	10.57	7
2122	CB	YHR	A	258	25.824	26.503	37.938	1.00	8.83	6	AT04	2175	CA	GLN	A	264	40.441	17.687	31.185	1.00	10.92	6
2123	CG1	YHR	A	258	25.203	27.678	38.617	1.00	7.38	8	AT04	2176	CB	GLN	A	264	40.619	16.999	32.536	1.00	18.66	6
2124	CG2	YHR	A	258	27.337	26.720	38.142	1.00	8.42	6	AT04	2177	CG	GLN	A	264	41.706	16.043	32.680	1.00	18.65	6
2125	C	YHR	A	258	26.136	25.533	35.646	1.00	8.29	6	AT04	2178	CD	GLN	A	264	41.972	15.344	33.934	1.00	23.60	6
2126	Q	YHR	A	258	25.764	24.341	35.656	1.00	8.22	7	AT04	2179	CE1	GLN	A	264	41.214	15.481	34.997	1.00	26.23	8
2127	H	VAL	A	259	27.160	25.972	34.922	1.00	7.82	7	AT04	2180	HE2	GLN	A	264	42.996	14.478	34.067	1.00	23.90	7
2128	CA	VAL	A	259	28.001	25.877	34.102	1.00	7.47	6	AT04	2181	C	GLN	A	264	39.681	16.811	30.191	1.00	11.04	6
2129	CB	VAL	A	259	27.859	25.175	32.566	1.00	5.00	6	AT04	2182	Q	GLN	A	264	38.461	16.643	30.232	1.00	10.83	8
2130	CG1	VAL	A	259	26.101	26.589	32.836	1.00	5.00	6	AT04	2183	H	ASN	A	265	40.454	16.216	29.289	1.00	11.25	7
2131	CG2	VAL	A	259	28.799	24.202	31.809	1.00	5.00	6	AT04	2184	CA	ASN	A	265	40.151	15.372	28.269	1.00	11.87	6
2132	C	VAL	A	259	29.428	25.381	34.552	1.00	7.58	6	AT04	2185	CB	ASN	A	265	41.223	15.365	27.078	1.00	11.52	6
2133	B	VAL	A	259	29.821	26.552	34.434	1.00	7.78	8	AT04	2186	CG	ASN	A	265	40.655	14.637	25.854	1.00	12.03	6
2134	H	ALA	A	260	30.181	24.348	34.913	1.00	7.84	7	AT04	2187	CB1	ASN	A	265	39.485	14.278	25.764	1.00	11.79	8
2135	CA	ALA	A	260	31.555	24.487	35.346	1.00	8.06	6	AT04	2188	H02	ASN	A	265	41.445	14.294	24.857	1.00	11.74	7
2136	CB	ALA	A	260	31.902	23.631	36.534	1.00	7.64	6	AT04	2189	C	ASN	A	265	40.028	13.873	28.691	1.00	12.36	6
2137	C	ALA	A	260	32.523	24.876	34.215	1.00	8.28	6	AT04	2190	Q	ASN	A	265	40.753	13.007	28.282	1.00	12.25	8
2138	Q	ALA	A	260	32.266	23.091	33.536	1.00	8.26	6	AT04	2191	H	ASN	A	266	39.136	13.476	29.634	1.00	13.06	7
2139	H	GLU	A	261	33.579	24.848	34.857	1.00	8.40	7	AT04	2192	CA	ASN	A	266	38.844	12.428	30.337	1.00	13.75	6
2140	CA	GLU	A	261	34.628	24.574	33.125	1.00	8.60	6	AT04	2193	CB	ASN	A	266	39.910	12.362	31.416	1.00	18.58	6
2141	CB	GLU	A	261	35.346	25.828	32.600	1.00	11.43	6	AT04	2194	CG	ASN	A	266	40.150	11.016	32.031	1.00	22.56	6
2142	CG	GLU	A	261	36.281	25.350	31.518	1.00	17.13	6	AT04	2195	H01	ASN	A	266	41.311	10.519	31.969	1.00	28.43	8
2143	CG1	GLU	A	261	36.823	26.339	30.525	1.00	23.18	6	AT04	2196	H02	ASN	A	266	39.160	10.410	32.462	1.00	21.13	7
2144	CG2	GLU	A	261	36.068	26.970	29.694	1.00	25.81	8	AT04	2197	C	ASN	A	266	37.441	12.394	30.944	1.00	13.73	6
2145	CE2	GLU	A	261	38.080	26.441	30.593	1.00	25.35	8	AT04	2198	Q	ASN	A	266	37.161	13.123	31.927	1.00	13.68	8
2146	C	GLU	A	261	35.844	31.459	33.867	1.00	9.48	6	AT04	2199	H	ALA	A	267	36.552	11.545	30.362	1.00	13.47	7
2147	Q	GLU	A	261	36.514	26.148	34.558	1.00	8.19	8	AT04	2200	CA	ALA	A	267	35.178	11.440	30.835	1.00	13.35	6
2148	H	YHR	A	262	35.578	22.360	33.710	1.00	8.54	7	AT04	2201	CB	ALA	A	267	34.330	10.532	29.944	1.00	12.56	6
2149	CA	YHR	A	262	36.500	21.367	34.293	1.00	8.87	6	AT04	2202	C	ALA	A	267	35.076	10.997	32.287	1.00	13.08	6
2150	CB	YHR	A	262	35.838	20.183	34.966	1.00	8.94	6	AT04	2203	Q	ALA	A	267	34.195	11.454	33.027	1.00	13.14	8
2151	CG	YHR	A	262	36.761	19.321	35.821	1.00	9.11	6	AT04	2204	H	GLY	A	268	35.918	10.106	32.733	1.00	12.97	7
2152	CD1	YHR	A	262	36.660	19.322	37.206	1.00	9.01	6	AT04	2205	CA	GLY	A	268	35.973	9.564	34.083	1.00	12.93	6
2153	CD1	YHR	A	262	37.509	18.576	37.984	1.00	9.15	6	AT04	2206	C	GLY	A	268	36.184	10.653	35.146	1.00	13.05	6
2154	CE2	YHR	A	262	37.743	18.497	35.253	1.00	9.44	6	AT04	2207	Q	GLY	A	268	35.512	10.656	36.213	1.00	13.01	8
2155	CE2	YHR	A	262	38.605	17.723	36.026	1.00	9.65	6	AT04	2208	CB	LYS	A	269	37.109	11.575	35.348	1.00	12.90	7
2156	CE2	YHR	A	262	38.590	17.788	37.424	1.00	9.42	6	AT04	2209	CA	LYS	A	269	37.425	12.681	35.786	1.00	13.04	6
2157	CH	YHR	A	262	39.303	17.012	38.214	1.00	9.41	8	AT04	2210	CB	LYS	A	269	38.790	13.296	35.417	1.00	17.63	6
2158	C	YHR	A	262	37.424	20.977	33.104	1.00	8.97	8	AT04	2211	CG	LYS	A	269	39.840	12.506	36.217	1.00	22.85	6
2159	Q	YHR	A	262	37.008	20.107	32.297	1.00	9.09	8	AT04	2212	CG	LYS	A	269	40.869	12.034	35.211	1.00	27.74	6
2160	H	HRP	A	263	38.590	21.592	32.945	1.00	9.15	7	AT04	2213	CE	LYS	A	269	41.722	10.885	35.785	1.00	30.85	6
2161	CA	HRP	A	263	39.403	21.292	31.774	1.00	9.76	6	AT04	2214	H1	LYS	A	269	42.663	10.356	34.698	1.00	32.73	7
2162	CB	HRP	A	263	40.193	22.560	31.346	1.00	9.45	6	AT04	2215	C	LYS	A	269	36.296	13.699	35.778	1.00	12.76	6
2163	CB	HRP	A	263	40.638	22.366	29.917	1.00	11.66	6	AT04	2216	Q	LYS	A	269	35.918	14.230	36.828	1.00	12.65	8
2164	CD2	HRP	A	263	39.892	22.703	28.733	1.00	12.75	6	AT04	2217	H	LEU	A	270	35.496	13.903	34.596	1.00	12.42	7
2165	CE2	HRP	A	263	40.662	22.299	27.612	1.00	13.78	6	AT04	2218	CA	LEU	A	270	34.164	13.161	33.088	1.00	13.16	6
2166	CE3	HRP	A	263	38.531	23.389	28.512	1.00	12.04	6	AT04	2219	CB	LEU	A	270	34.539	14.810	34.538	1.00	13.49	6
2167	CD1	HRP	A	263	41.800	21.810	29.466	1.00	12.57	6	AT04	2220	CG	LEU	A	270	34.959	16.348	32.467	1.00	13.12	6
2168	HE1	HRP	A	263	41.830	21.731	28.078	1.00	13.80	7	AT04	2221	CH1	LEU	A	270	34.614	17.623	33.197	1.00	13.42	6
2169	CD2	HRP	A	263	40.305	22.513	26.299	1.00	14.12	6	AT04	2222	CD2	LEU	A	270	36.465	16.210	32.558	1.00	13.72	6
2170	CD3	HRP	A	263	38.201	23.453	27.210	1.00	11.77	6	AT04	2223	C	LEU	A	270	33.412	14.169	33.315	1.00	11.76	6
2171	CH2	HRP	A	263	38.970	23.094	26.122	1.00	11.88	6	AT04	2224	H	LEU	A	270	32.700	14.934	33.981	1.00	11.83	8
2172	C	HRP	A	263	40.303	20.053	31.833	1.00	10.24	6	AT04	2225	H	GLU	A	271	33.219	12.851	35.281	1.00	11.41	7
2173	Q	HRP	A	263	41.436	20.018	32.294	1.00	10.30	8	AT04	2226	CA	GLU	A	271	32.136	12.253	36.051	1.00	11.29	6

2227	CB	GLU A 271	32.024	10.817	35.510	1.00	16.08	6	2280	CA	THR A 277	29.173	18.167	43.406	1.00	12.78	6
2228	CG	GLU A 271	31.015	10.010	34.333	1.00	21.09	6	2281	CB	THR A 277	29.520	19.264	42.357	1.00	12.02	6
2229	CD	GLU A 271	30.661	8.827	33.720	1.00	27.19	6	2282	CG2	THR A 277	29.323	18.649	41.065	1.00	12.30	8
2230	CE1	GLU A 271	29.716	8.351	35.359	1.00	29.23	8	2283	CG2	THR A 277	30.941	19.791	42.492	1.00	8.90	6
2231	CE2	GLU A 271	31.830	7.845	35.526	1.00	30.01	8	2284	C	THR A 277	27.701	17.794	43.416	1.00	12.70	6
2232	C	GLU A 271	32.339	12.729	37.534	1.00	10.89	6	2285	O	THR A 277	26.812	18.613	43.190	1.00	12.66	8
2233	O	GLU A 271	31.458	12.370	38.404	1.00	10.58	8	2286	N	SER A 278	27.426	16.518	43.673	1.00	12.73	7
2234	N	ASH A 272	33.615	12.189	37.987	1.00	10.66	7	2287	CA	SER A 278	26.869	16.047	43.729	1.00	12.83	6
2235	CA	ASH A 272	34.008	12.309	39.385	1.00	10.31	6	2288	CB	SER A 278	25.280	16.884	44.854	1.00	14.69	6
2236	CB	ASH A 272	35.520	12.089	39.643	1.00	11.32	6	2289	CG	SER A 278	25.963	16.531	46.061	1.00	18.04	8
2237	CG	ASH A 272	35.969	12.380	41.064	1.00	11.99	6	2290	C	SER A 278	25.283	16.294	42.474	1.00	12.85	6
2238	CO1	ASH A 272	35.616	11.803	41.964	1.00	11.66	8	2291	O	SER A 278	24.049	16.483	42.663	1.00	13.07	8
2239	CO2	ASH A 272	36.701	13.674	41.322	1.00	12.45	7	2292	N	PHE A 279	25.774	16.339	41.260	1.00	12.49	7
2240	C	ASH A 272	33.588	13.709	39.873	1.00	9.78	6	2293	CA	PHE A 279	24.897	16.523	40.100	1.00	12.16	6
2241	O	ASH A 272	33.080	13.897	40.979	1.00	9.63	8	2294	CB	PHE A 279	23.976	15.344	39.973	1.00	12.70	6
2242	N	THR A 273	35.777	14.748	39.063	1.00	9.45	7	2295	CG	PHE A 279	24.772	14.122	39.524	1.00	12.87	6
2243	CA	THR A 273	33.349	16.104	39.486	1.00	9.06	6	2296	CD1	PHE A 279	25.183	13.153	40.435	1.00	13.85	6
2244	CB	THR A 273	33.908	17.179	38.558	1.00	8.65	6	2297	CD2	PHE A 279	25.085	13.919	38.199	1.00	13.30	6
2245	CG	THR A 273	33.509	18.626	38.903	1.00	8.44	6	2298	CE1	PHE A 279	25.903	12.038	40.045	1.00	13.14	6
2246	CO1	THR A 273	34.242	19.333	39.838	1.00	8.51	6	2299	CE2	PHE A 279	25.801	13.799	37.786	1.00	13.99	6
2247	CE1	THR A 273	33.915	20.650	40.228	1.00	8.39	6	2300	CZ	PHE A 279	26.244	11.878	38.726	1.00	13.30	6
2248	CE2	THR A 273	32.591	19.231	38.364	1.00	8.33	6	2301	C	PHE A 279	24.170	17.912	40.149	1.00	12.03	6
2249	CE2	THR A 273	32.015	20.523	38.895	1.00	8.66	6	2302	O	PHE A 279	23.185	16.072	39.417	1.00	12.27	8
2250	CZ	THR A 273	32.627	21.214	39.625	1.00	8.60	6	2303	N	ASH A 280	24.644	18.942	40.882	1.00	11.58	7
2251	OH	THR A 273	32.452	22.481	39.938	1.00	8.94	8	2304	CA	ASH A 280	23.979	20.238	40.984	1.00	11.30	6
2252	C	THR A 273	31.837	16.135	39.662	1.00	9.06	6	2305	CG	ASH A 280	24.025	20.735	42.438	1.00	11.18	6
2253	O	THR A 273	31.340	16.679	40.688	1.00	8.80	8	2306	CB	ASH A 280	25.222	21.558	42.868	1.00	13.48	6
2254	N	LEU A 274	31.061	15.569	38.736	1.00	9.52	7	2307	CO1	ASH A 280	26.142	21.809	42.087	1.00	12.89	8
2255	CA	LEU A 274	29.590	15.550	38.849	1.00	10.16	6	2308	CO2	ASH A 280	25.289	22.094	44.111	1.00	12.18	7
2256	CB	LEU A 274	28.901	14.856	37.646	1.00	10.22	6	2309	C	ASH A 280	24.632	21.267	39.927	1.00	10.94	6
2257	CG	LEU A 274	29.158	15.528	36.280	1.00	10.91	6	2310	O	ASH A 280	23.910	22.353	39.820	1.00	11.03	8
2258	CO1	LEU A 274	28.719	14.634	35.107	1.00	11.67	6	2311	N	GLU A 281	25.325	20.890	39.032	1.00	10.60	7
2259	CO2	LEU A 274	28.532	16.863	34.196	1.00	10.03	6	2312	CA	GLU A 281	25.784	21.736	37.949	1.00	10.04	6
2260	C	LEU A 274	29.157	14.918	40.173	1.00	10.59	6	2313	CB	GLU A 281	26.930	22.636	38.400	1.00	9.98	6
2261	O	LEU A 274	28.353	15.463	40.920	1.00	10.27	8	2314	CG	GLU A 281	28.117	21.977	39.038	1.00	9.72	6
2262	N	ASH A 275	29.706	13.730	40.471	1.00	11.45	7	2315	CO	GLU A 281	29.055	22.863	39.859	1.00	9.08	6
2263	CA	ASH A 275	29.463	13.009	41.709	1.00	12.37	6	2316	OE1	GLU A 281	30.064	23.342	39.150	1.00	8.97	6
2264	CB	ASH A 275	29.287	11.694	41.835	1.00	19.11	6	2317	OE2	GLU A 281	28.835	23.085	41.151	1.00	8.05	7
2265	CG	ASH A 275	29.761	10.565	40.962	1.00	24.07	6	2318	C	GLU A 281	26.239	20.871	38.771	1.00	9.66	6
2266	CO1	ASH A 275	28.743	9.915	41.314	1.00	27.53	8	2319	O	GLU A 281	26.615	19.783	36.902	1.00	9.22	8
2267	CO2	ASH A 275	30.352	10.254	39.805	1.00	10.27	7	2320	N	SER A 282	26.224	21.522	35.616	1.00	9.14	7
2268	C	ASH A 275	29.820	13.870	42.924	1.00	12.34	6	2321	CA	SER A 282	26.674	20.851	34.389	1.00	8.74	6
2269	O	ASH A 275	28.964	14.072	43.781	1.00	12.19	8	2322	CB	SER A 282	25.985	21.419	33.131	1.00	7.22	6
2270	N	LYS A 276	31.008	14.435	43.005	1.00	12.51	7	2323	CG	SER A 282	24.607	21.123	33.102	1.00	6.53	8
2271	CA	LYS A 276	31.661	15.251	44.130	1.00	12.99	6	2324	C	SER A 282	28.170	21.077	34.201	1.00	8.54	6
2272	CB	LYS A 276	32.952	15.885	44.000	1.00	12.82	6	2325	O	SER A 282	28.773	21.913	34.919	1.00	8.89	8
2273	CG	LYS A 276	33.825	14.366	44.050	1.00	13.95	6	2326	N	VAL A 283	28.777	20.420	33.240	1.00	8.11	7
2274	CO	LYS A 276	33.535	13.485	45.269	1.00	14.29	6	2327	CA	VAL A 283	30.154	20.596	32.841	1.00	7.98	6
2275	CE	LYS A 276	34.141	12.103	45.203	1.00	13.18	6	2328	CB	VAL A 283	31.137	19.443	33.210	1.00	8.54	6
2276	CD	LYS A 276	35.602	12.078	44.906	1.00	13.50	7	2329	CG1	VAL A 283	31.457	19.441	34.708	1.00	9.20	6
2277	K2	LYS A 276	30.851	16.533	44.311	1.00	13.25	6	2330	CG2	VAL A 283	30.599	16.117	32.719	1.00	7.85	6
2278	O	LYS A 276	30.650	17.117	45.412	1.00	13.74	8	2331	C	VAL A 283	30.218	20.758	31.304	1.00	7.87	6
2279	N	THR A 277	29.966	16.979	43.256	1.00	12.99	7	2332	O	VAL A 283	29.342	20.263	30.572	1.00	7.75	8

2333	W	PHE A 284	31.212	21.483	30.801	1.00	7.72	7	1.00	7.08	6
2334	CA	PHE A 284	31.460	21.589	29.383	1.00	7.67	6	1.00	7.95	6
2335	CB	PHE A 284	32.518	22.669	29.110	1.00	7.48	6	1.00	7.13	6
2336	CG	PHE A 284	31.953	26.060	29.268	1.00	7.61	6	1.00	9.46	6
2337	CD	PHE A 284	32.301	24.886	30.277	1.00	6.90	6	1.00	8.24	6
2338	CE	PHE A 284	31.062	26.475	30.252	1.00	7.80	6	1.00	9.38	6
2339	CE1	PHE A 284	31.782	26.187	30.312	1.00	8.33	6	1.00	9.13	6
2340	CE2	PHE A 284	30.501	25.756	28.282	1.00	6.48	6	1.00	8.42	6
2341	CE	PHE A 284	30.882	26.602	29.314	1.00	7.74	6	1.00	8.61	8
2342	C	PHE A 284	31.997	20.212	28.924	1.00	7.66	6	1.00	8.43	7
2343	O	PHE A 284	32.833	19.541	29.627	1.00	7.52	8	1.00	8.66	6
2344	H	ASP A 285	31.517	19.758	27.741	1.00	7.99	7	1.00	8.44	6
2345	CA	ASP A 285	31.997	18.432	27.212	1.00	8.11	6	1.00	8.91	6
2346	CB	ASP A 285	30.919	17.867	26.269	1.00	8.64	6	1.00	8.93	8
2347	CG	ASP A 285	31.063	16.361	26.096	1.00	9.93	6	1.00	8.51	7
2348	CD	ASP A 285	32.173	15.774	26.289	1.00	8.07	8	1.00	8.93	6
2349	CE	ASP A 285	30.024	15.731	25.749	1.00	9.24	8	1.00	8.32	8
2350	C	ASP A 285	33.339	18.591	26.496	1.00	8.25	6	1.00	9.66	7
2351	O	ASP A 285	33.394	18.729	25.236	1.00	8.58	8	1.00	10.70	6
2352	H	VAL A 286	34.668	18.590	27.218	1.00	7.95	7	1.00	11.55	6
2353	CA	VAL A 286	35.813	18.709	26.644	1.00	7.80	6	1.00	12.98	6
2354	CB	VAL A 286	36.851	18.934	27.764	1.00	7.80	6	1.00	10.98	6
2355	CG	VAL A 286	38.370	19.085	27.261	1.00	5.55	6	1.00	11.27	6
2356	CD	VAL A 286	36.518	20.231	28.524	1.00	8.40	6	1.00	11.19	6
2357	C	VAL A 286	36.145	17.549	25.719	1.00	7.74	6	1.00	11.27	8
2358	O	VAL A 286	36.811	17.833	24.601	1.00	7.94	8	1.00	11.50	7
2359	H	PRO A 287	35.967	16.276	26.097	1.00	7.41	7	1.00	12.28	6
2360	CD	PRO A 287	35.495	15.854	27.613	1.00	7.11	6	1.00	13.35	6
2361	CA	PRO A 287	36.262	15.131	25.226	1.00	7.24	6	1.00	13.35	6
2362	CB	PRO A 287	35.802	13.885	25.970	1.00	7.14	6	1.00	13.35	6
2363	CG	PRO A 287	35.741	14.357	27.394	1.00	7.12	6	1.00	13.35	6
2364	C	PRO A 287	35.589	15.313	23.873	1.00	7.43	6	1.00	13.35	6
2365	O	PRO A 287	36.214	15.115	22.634	1.00	7.51	8	1.00	13.35	6
2366	H	LEU A 288	34.293	15.681	23.762	1.00	7.34	7	1.00	12.05	8
2367	CA	LEU A 288	33.608	15.904	22.504	1.00	7.34	6	1.00	12.05	8
2368	CB	LEU A 288	32.349	16.325	22.654	1.00	7.25	6	1.00	12.05	8
2369	CG	LEU A 288	31.438	16.481	21.283	1.00	8.35	6	1.00	12.37	6
2370	CD	LEU A 288	31.384	15.185	20.494	1.00	8.34	6	1.00	12.51	6
2371	CE	LEU A 288	30.038	16.988	21.510	1.00	5.28	6	1.00	13.89	6
2372	C	LEU A 288	34.329	16.998	21.722	1.00	7.39	6	1.00	13.85	7
2373	O	LEU A 288	34.398	16.793	20.525	1.00	7.49	8	1.00	13.85	7
2374	H	GLN A 293	34.847	18.097	22.260	1.00	7.34	7	1.00	13.85	6
2375	CA	GLN A 293	35.583	19.114	22.445	1.00	7.21	6	1.00	13.85	6
2376	CB	GLN A 293	34.094	20.240	22.445	1.00	5.61	6	1.00	13.85	6
2377	CG	GLN A 293	37.215	21.083	21.852	1.00	5.00	6	1.00	13.85	6
2378	CD	GLN A 293	36.548	21.040	22.012	1.00	5.00	6	1.00	13.85	6
2379	CE	GLN A 293	36.966	22.086	20.914	1.00	5.00	7	1.00	13.85	6
2380	C	GLN A 293	38.127	22.570	20.527	1.00	5.00	6	1.00	13.85	6
2381	H	GLN A 293	39.124	21.983	21.176	1.00	5.00	7	1.00	13.85	6
2382	D	GLN A 293	36.776	18.507	20.805	1.00	7.52	6	1.00	13.85	6
2383	D	GLN A 293	37.083	18.809	19.647	1.00	7.41	8	1.00	13.85	6
2384	H	PHE A 290	37.518	17.654	21.545	1.00	7.75	7	1.00	13.85	6
2385	CA	PHE A 290	38.721	16.971	21.050	1.00	8.12	6	1.00	13.85	6
2386	CB	PHE A 290	39.575	16.332	22.175	1.00	7.08	6	1.00	13.85	6
2387	CG	PHE A 290	40.370	17.378	22.893	1.00	7.95	6	1.00	13.85	6
2388	CD	PHE A 290	40.054	17.819	24.152	1.00	7.13	6	1.00	13.85	6
2389	CE	PHE A 290	41.831	18.012	22.214	1.00	9.46	6	1.00	13.85	6
2390	CE1	PHE A 290	40.764	18.810	24.791	1.00	8.24	6	1.00	13.85	6
2391	CE2	PHE A 290	42.137	19.075	22.838	1.00	9.38	6	1.00	13.85	6
2392	C	PHE A 290	41.830	19.458	24.125	1.00	9.13	6	1.00	13.85	6
2393	O	PHE A 290	38.341	15.943	19.084	1.00	8.42	6	1.00	13.85	6
2394	H	ASP A 291	39.158	15.881	19.025	1.00	8.61	8	1.00	13.85	6
2395	CA	ASP A 291	37.239	15.234	20.127	1.00	8.43	7	1.00	13.85	6
2396	CB	ASP A 291	36.826	14.303	19.077	1.00	8.66	6	1.00	13.85	6
2397	CG	ASP A 291	35.581	13.461	19.414	1.00	9.01	6	1.00	13.85	6
2398	CD	ASP A 291	35.866	12.427	20.305	1.00	10.93	6	1.00	13.85	6
2399	CE	ASP A 291	37.040	12.332	20.954	1.00	10.93	8	1.00	13.85	6
2400	C	ASP A 291	34.848	11.690	20.917	1.00	8.51	7	1.00	13.85	6
2401	H	ASP A 291	34.507	15.080	17.798	1.00	8.93	6	1.00	13.85	6
2402	O	ASP A 291	36.824	14.630	16.701	1.00	8.32	8	1.00	13.85	6
2403	H	LEU A 292	35.808	16.219	17.925	1.00	9.66	7	1.00	13.85	6
2404	CA	LEU A 292	35.459	17.043	16.777	1.00	10.70	6	1.00	13.85	6
2405	CB	LEU A 292	34.525	18.280	17.143	1.00	11.55	6	1.00	13.85	6
2406	CG	LEU A 292	33.126	17.717	17.616	1.00	12.98	6	1.00	13.85	6
2407	CD	LEU A 292	32.406	18.847	18.358	1.00	10.98	6	1.00	13.85	6
2408	CE	LEU A 292	32.371	17.124	16.439	1.00	11.27	6	1.00	13.85	6
2409	C	LEU A 292	34.713	17.628	16.088	1.00	11.19	6	1.00	13.85	6
2410	O	LEU A 292	34.831	17.685	14.878	1.00	11.27	8	1.00	13.85	6
2411	H	GLN A 293	37.674	18.093	16.832	1.00	11.50	7	1.00	13.85	6
2412	CA	GLN A 293	38.899	18.619	16.322	1.00	12.28	6	1.00	13.85	6
2413	CB	GLN A 293	39.632	19.090	17.572	1.00	13.35	6	1.00	13.85	6
2414	CG	GLN A 293	40.644	20.159	17.294	1.00	20.28	6	1.00	13.85	6
2415	CD	GLN A 293	42.018	19.550	17.111	1.00	23.63	6	1.00	13.85	6
2416	CE	GLN A 293	42.277	18.617	17.083	1.00	27.19	8	1.00	13.85	6
2417	C	GLN A 293	42.755	20.086	16.154	1.00	25.26	7	1.00	13.85	6
2418	O	GLN A 293	39.771	17.574	15.581	1.00	12.47	6	1.00	13.85	6
2419	H	ALA A 294	40.434	17.827	14.578	1.00	12.05	8	1.00	13.85	6
2420	CA	ALA A 294	39.793	16.376	16.196	1.00	12.05	8	1.00	13.85	6
2421	CB	ALA A 294	40.537	15.278	15.855	1.00	13.37	6	1.00	13.85	6
2422	CG	ALA A 294	40.630	14.069	16.583	1.00	12.51	6	1.00	13.85	6
2423	CD	ALA A 294	39.929	14.904	14.299	1.00	13.89	6	1.00	13.85	6
2424	CE	ALA A 294	40.681	14.764	13.312	1.00	16.17	8	1.00	13.85	6
2425	C	ALA A 294	38.580	14.604	14.165	1.00	13.85	7	1.00	13.85	6
2426	CA	ALA A 295	37.963	14.486	12.906	1.00	13.85	6	1.00	13.85	6
2427	CB	ALA A 295	36.457	14.351	12.963	1.00	13.85	6	1.00	13.85	6
2428	CG	ALA A 295	38.289	15.586	11.874	1.00	16.11	6	1.00	13.85	6
2429	CD	ALA A 295	38.474	15.301	10.878	1.00	16.15	8	1.00	13.85	6
2430	C	ALA A 295	38.311	16.645	12.332	1.00	16.08	7	1.00	13.85	6
2431	H	ALA A 296	38.562	17.954	11.422	1.00	16.17	6	1.00	13.85	6
2432	CA	ALA A 296	39.176	19.868	12.887	1.00	10.42	6	1.00	13.85	6
2433	CB	ALA A 296	38.176	19.248	12.187	1.00	10.42	6	1.00	13.85	6
2434	CG	ALA A 296	40.000	17.997	10.859	1.00	14.43	6	1.00	13.85	6
2435	CD	ALA A 296	40.338	18.622	9.818	1.00	14.12	8	1.00	13.85	6
2436	C	ALA A 297	40.992	17.322	11.540	1.00	14.82	7	1.00	13.85	6
2437	CA	ALA A 297	42.305	17.287	11.269	1.00	15.50	6	1.00	13.85	6
2438	CB	ALA A 297	42.931	16.991	12.708	1.00	16.67	6	1.00	13.85	6

2545	Q	THR A 311	30.667	10.902	27.258	1.00	11.29	8
2546	R	VAL A 312	31.198	13.075	27.543	1.00	11.20	7
2547	CA	VAL A 312	30.513	13.282	28.403	1.00	11.29	6
2548	CB	VAL A 312	30.567	14.437	29.407	1.00	12.62	6
2549	CG1	VAL A 312	29.820	14.906	30.597	1.00	13.45	6
2550	CG2	VAL A 312	31.095	14.730	29.912	1.00	10.56	6
2551	C	VAL A 312	28.874	13.189	28.191	1.00	11.23	6
2552	Q	VAL A 313	28.053	12.526	28.793	1.00	11.01	8
2553	R	VAL A 313	28.533	13.825	27.061	1.00	11.42	7
2554	CA	VAL A 313	27.208	13.790	28.498	1.00	11.94	6
2555	CB	VAL A 313	27.107	14.723	25.268	1.00	12.88	6
2556	CG1	VAL A 313	27.604	14.175	23.962	1.00	13.11	6
2557	CG2	VAL A 313	25.627	15.102	23.180	1.00	14.06	6
2558	C	VAL A 313	26.655	12.380	26.319	1.00	12.21	6
2559	Q	VAL A 314	25.434	12.216	26.319	1.00	11.60	8
2560	R	VAL A 314	27.418	11.313	25.971	1.00	12.83	7
2561	CA	VAL A 314	26.878	9.987	25.750	1.00	13.56	6
2562	CB	VAL A 314	27.801	9.054	24.932	1.00	13.63	6
2563	CG	VAL A 314	29.056	9.048	25.841	1.00	15.90	8
2564	C	VAL A 314	26.572	9.345	27.111	1.00	14.04	6
2565	Q	VAL A 315	25.730	8.445	27.105	1.00	14.28	8
2566	R	VAL A 315	27.168	9.725	28.254	1.00	14.23	7
2567	CA	VAL A 315	26.823	9.081	29.513	1.00	14.22	6
2568	CB	VAL A 315	27.928	8.797	30.491	1.00	19.81	6
2569	CG	VAL A 315	29.333	8.495	30.319	1.00	26.75	6
2570	C	VAL A 315	30.321	9.481	30.402	1.00	32.49	6
2571	Q	VAL A 316	30.714	10.114	31.825	1.00	35.30	6
2572	R	VAL A 316	31.599	9.199	32.634	1.00	35.57	7
2573	CA	VAL A 316	25.684	9.951	30.379	1.00	13.74	6
2574	CB	VAL A 316	24.969	9.435	31.020	1.00	13.60	7
2575	CG	VAL A 316	26.108	11.257	30.397	1.00	13.12	7
2576	C	VAL A 316	25.314	12.197	31.129	1.00	13.02	6
2577	Q	VAL A 316	26.202	12.791	32.327	1.00	12.69	6
2578	R	VAL A 316	26.558	11.718	33.313	1.00	12.94	6
2579	CA	VAL A 316	25.796	11.024	34.166	1.00	13.25	6
2580	CB	VAL A 316	27.835	11.194	33.424	1.00	15.42	7
2581	CG	VAL A 316	27.850	10.206	34.317	1.00	14.97	6
2582	C	VAL A 316	26.617	10.106	34.822	1.00	15.47	7
2583	Q	VAL A 316	24.609	13.360	30.323	1.00	12.44	6
2584	R	VAL A 316	25.304	14.479	30.471	1.00	12.29	8
2585	CA	VAL A 317	23.868	13.075	29.435	1.00	12.52	7
2586	CB	VAL A 317	23.254	11.740	29.268	1.00	12.50	6
2587	CG	VAL A 317	23.311	14.040	28.519	1.00	12.50	6
2588	C	VAL A 317	22.280	13.268	27.640	1.00	12.54	6
2589	Q	VAL A 317	21.996	12.031	28.584	1.00	12.54	6
2590	R	VAL A 317	22.669	15.253	29.133	1.00	12.59	6
2591	CA	VAL A 317	22.750	16.349	28.542	1.00	12.88	8
2592	CB	VAL A 317	22.033	15.168	30.956	1.00	12.44	7
2593	CG	VAL A 317	21.370	16.286	30.956	1.00	12.38	6
2594	C	VAL A 317	20.278	15.805	31.970	1.00	13.77	6
2595	Q	VAL A 318	18.250	14.143	32.261	1.00	15.85	6
2596	R	VAL A 318	18.520	15.629	30.254	1.00	15.19	6
2597	CA	VAL A 318	18.520	15.629	30.254	1.00	15.19	6
2598	CB	VAL A 318	18.520	15.629	30.254	1.00	15.19	6
2599	CG	VAL A 318	18.520	15.629	30.254	1.00	15.19	6
2600	C	VAL A 318	18.520	15.629	30.254	1.00	15.19	6
2601	Q	VAL A 319	18.520	15.629	30.254	1.00	15.19	6
2602	R	VAL A 319	18.520	15.629	30.254	1.00	15.19	6
2603	CA	VAL A 319	18.520	15.629	30.254	1.00	15.19	6
2604	CB	VAL A 319	18.520	15.629	30.254	1.00	15.19	6
2605	CG	VAL A 319	18.520	15.629	30.254	1.00	15.19	6
2606	C	VAL A 319	18.520	15.629	30.254	1.00	15.19	6
2607	Q	VAL A 319	18.520	15.629	30.254	1.00	15.19	6
2608	R	VAL A 319	18.520	15.629	30.254	1.00	15.19	6
2609	CA	VAL A 320	18.520	15.629	30.254	1.00	15.19	6
2610	CB	VAL A 320	18.520	15.629	30.254	1.00	15.19	6
2611	CG	VAL A 320	18.520	15.629	30.254	1.00	15.19	6
2612	C	VAL A 320	18.520	15.629	30.254	1.00	15.19	6
2613	Q	VAL A 320	18.520	15.629	30.254	1.00	15.19	6
2614	R	VAL A 320	18.520	15.629	30.254	1.00	15.19	6
2615	CA	VAL A 321	18.520	15.629	30.254	1.00	15.19	6
2616	CB	VAL A 321	18.520	15.629	30.254	1.00	15.19	6
2617	CG	VAL A 321	18.520	15.629	30.254	1.00	15.19	6
2618	C	VAL A 321	18.520	15.629	30.254	1.00	15.19	6
2619	Q	VAL A 321	18.520	15.629	30.254	1.00	15.19	6
2620	R	VAL A 321	18.520	15.629	30.254	1.00	15.19	6
2621	CA	VAL A 322	18.520	15.629	30.254	1.00	15.19	6
2622	CB	VAL A 322	18.520	15.629	30.254	1.00	15.19	6
2623	CG	VAL A 322	18.520	15.629	30.254	1.00	15.19	6
2624	C	VAL A 322	18.520	15.629	30.254	1.00	15.19	6
2625	Q	VAL A 322	18.520	15.629	30.254	1.00	15.19	6
2626	R	VAL A 322	18.520	15.629	30.254	1.00	15.19	6
2627	CA	VAL A 323	18.520	15.629	30.254	1.00	15.19	6
2628	CB	VAL A 323	18.520	15.629	30.254	1.00	15.19	6
2629	CG	VAL A 323	18.520	15.629	30.254	1.00	15.19	6
2630	C	VAL A 323	18.520	15.629	30.254	1.00	15.19	6
2631	Q	VAL A 323	18.520	15.629	30.254	1.00	15.19	6
2632	R	VAL A 323	18.520	15.629	30.254	1.00	15.19	6
2633	CA	VAL A 323	18.520	15.629	30.254	1.00	15.19	6
2634	CB	VAL A 323	18.520	15.629	30.254	1.00	15.19	6
2635	CG	VAL A 323	18.520	15.629	30.254	1.00	15.19	6
2636	C	VAL A 323	18.520	15.629	30.254	1.00	15.19	6
2637	Q	VAL A 323	18.520	15.629	30.254	1.00	15.19	6
2638	R	VAL A 324	18.520	15.629	30.254	1.00	15.19	6
2639	CA	VAL A 324	18.520	15.629	30.254	1.00	15.19	6
2640	CB	VAL A 324	18.520	15.629	30.254	1.00	15.19	6
2641	CG	VAL A 324	18.520	15.629	30.254	1.00	15.19	6
2642	C	VAL A 324	18.520	15.629	30.254	1.00	15.19	6
2643	Q	VAL A 324	18.520	15.629	30.254	1.00	15.19	6
2644	R	VAL A 324	18.520	15.629	30.254	1.00	15.19	6
2645	CA	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2646	CB	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2647	CG	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2648	C	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2649	Q	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2650	R	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2651	CA	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2652	CB	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2653	CG	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2654	C	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2655	Q	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2656	R	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2657	CA	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2658	CB	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2659	CG	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2660	C	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2661	Q	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2662	R	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2663	CA	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2664	CB	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2665	CG	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2666	C	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2667	Q	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2668	R	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2669	CA	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2670	CB	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2671	CG	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2672	C	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2673	Q	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2674	R	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2675	CA	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2676	CB	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2677	CG	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2678	C	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2679	Q	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2680	R	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2681	CA	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2682	CB	VAL A 325	18.520	15.629	30.254	1.00	15.19	6
2683								

2651	001 ASP A 325	38.076	25.409	18.839	1.00	7.66	8	2704	N	GLY A 332	46.122	30.693	18.593	1.00	15.77	7
2652	002 ASP A 325	37.027	25.682	16.964	1.00	9.34	8	2705	CA	GLY A 332	47.087	31.634	19.404	1.00	17.06	6
2653	003 ASP A 325	35.117	27.261	21.116	1.00	8.18	6	2706	C	GLY A 332	46.881	31.663	20.896	1.00	18.22	6
2654	004 ASP A 325	33.960	27.635	21.254	1.00	8.16	8	2707	O	GLY A 332	47.755	31.915	21.633	1.00	18.26	8
2655	005 ASP A 326	36.188	27.788	21.828	1.00	8.35	7	2708	N	GLY A 333	45.817	30.862	21.429	1.00	19.04	7
2656	006 ASP A 326	35.925	28.645	22.813	1.00	8.28	6	2709	CA	GLY A 333	45.678	30.778	22.875	1.00	19.88	6
2657	007 ASP A 326	35.487	28.329	24.160	1.00	9.54	6	2710	CB	GLY A 333	44.181	30.830	23.241	1.00	19.70	6
2658	008 ASP A 326	36.502	27.485	24.902	1.00	11.91	6	2711	CG	GLY A 333	43.711	32.283	23.072	1.00	20.78	6
2659	009 ASP A 326	37.701	27.415	24.622	1.00	12.52	8	2712	CG	GLY A 333	44.572	33.254	23.876	1.00	23.47	6
2660	010 ASP A 326	36.121	28.782	25.985	1.00	11.95	7	2713	OE1	GLY A 333	45.181	34.191	23.315	1.00	26.12	8
2661	011 ASP A 326	37.212	29.685	22.871	1.00	8.44	6	2714	OE2	GLY A 333	44.705	33.056	25.175	1.00	22.30	7
2662	012 ASP A 326	38.140	29.601	22.053	1.00	7.98	8	2715	C	GLY A 333	46.462	29.622	23.446	1.00	20.87	6
2663	013 ASP A 327	37.266	30.626	23.836	1.00	8.65	7	2716	O	GLY A 333	47.167	28.850	22.773	1.00	20.84	8
2664	014 ASP A 327	38.367	31.562	23.994	1.00	9.17	6	2717	N	SEK A 334	46.339	29.553	24.795	1.00	21.65	7
2665	015 ASP A 327	37.976	32.718	24.999	1.00	8.48	6	2718	CA	SEK A 334	47.083	28.519	25.552	1.00	22.42	6
2666	016 ASP A 327	37.800	32.154	26.392	1.00	7.81	6	2719	CB	SEK A 334	46.792	28.705	27.067	1.00	26.55	6
2667	017 ASP A 327	38.481	32.357	27.533	1.00	7.34	6	2720	OE	SEK A 334	45.405	29.089	27.235	1.00	30.85	8
2668	018 ASP A 327	36.785	31.222	26.872	1.00	6.46	7	2721	O	SEK A 334	47.687	26.393	24.929	1.00	22.55	8
2669	019 ASP A 327	36.886	30.856	27.951	1.00	7.98	6	2722	O	SEK A 334	45.506	26.728	25.170	1.00	21.74	7
2670	020 ASP A 327	37.683	31.538	28.493	1.00	8.30	7	2723	N	LEU A 335	44.958	25.411	24.863	1.00	20.75	6
2671	021 ASP A 327	39.664	30.065	24.404	1.00	9.58	6	2724	CA	LEU A 335	43.814	25.183	25.883	1.00	22.84	6
2672	022 ASP A 327	40.710	31.444	26.169	1.00	9.63	8	2725	CB	LEU A 335	44.252	25.266	27.365	1.00	23.70	6
2673	023 ASP A 328	39.645	29.653	24.928	1.00	10.53	7	2726	CG	LEU A 335	43.065	25.292	28.305	1.00	23.07	6
2674	024 ASP A 328	40.783	28.869	25.312	1.00	10.53	6	2727	CO1	LEU A 335	45.184	24.089	27.673	1.00	24.51	6
2675	025 ASP A 328	40.422	27.735	26.332	1.00	14.56	6	2728	CO2	LEU A 335	44.460	25.313	23.427	1.00	19.68	8
2676	026 ASP A 328	39.676	27.936	27.629	1.00	18.50	6	2729	C	LEU A 335	43.691	24.609	23.136	1.00	19.77	8
2677	027 ASP A 328	40.162	28.843	28.385	1.00	17.22	8	2730	O	LEU A 335	45.111	26.053	22.536	1.00	18.47	7
2678	028 ASP A 328	38.615	27.265	28.055	1.00	18.97	8	2731	N	GLU A 336	44.766	24.089	21.149	1.00	17.45	6
2679	029 ASP A 328	41.365	28.188	24.074	1.00	10.65	6	2732	CA	GLU A 336	45.908	26.773	20.387	1.00	19.49	6
2680	030 ASP A 328	42.607	28.841	23.933	1.00	10.58	8	2733	CB	GLU A 336	45.655	26.544	18.905	1.00	22.99	6
2681	031 ASP A 329	40.518	27.688	23.167	1.00	18.47	7	2734	CG	GLU A 336	46.276	27.487	16.805	1.00	28.18	8
2682	032 ASP A 329	40.946	26.880	22.028	1.00	10.37	6	2735	CO	GLU A 336	47.378	28.166	18.504	1.00	26.94	8
2683	033 ASP A 329	39.933	25.709	21.777	1.00	10.26	6	2736	OE1	GLU A 336	44.504	24.698	20.571	1.00	16.40	6
2684	034 ASP A 329	39.596	24.873	23.020	1.00	9.29	6	2737	OE2	GLU A 336	45.349	23.802	20.847	1.00	18.09	8
2685	035 ASP A 329	41.142	27.596	20.702	1.00	10.36	6	2738	O	GLU A 336	43.138	23.527	19.954	1.00	15.33	7
2686	036 ASP A 329	41.563	26.999	19.704	1.00	9.94	6	2739	N	SEK A 337	43.005	23.217	19.393	1.00	14.23	6
2687	037 ASP A 329	40.827	28.878	20.679	1.00	10.77	7	2740	CA	SEK A 337	42.891	22.175	20.487	1.00	13.68	8
2688	038 ASP A 330	40.985	29.688	19.441	1.00	11.30	6	2741	CB	SEK A 337	41.855	22.515	21.439	1.00	13.96	8
2689	039 ASP A 330	40.749	31.987	20.543	1.00	8.40	6	2742	CG	SEK A 337	41.679	23.436	18.645	1.00	13.82	6
2690	040 ASP A 330	40.603	33.322	20.559	1.00	8.44	6	2743	C	SEK A 337	40.815	22.864	18.896	1.00	13.57	8
2691	041 ASP A 330	40.749	31.987	20.543	1.00	8.40	6	2744	O	SEK A 337	40.815	22.864	18.896	1.00	13.57	8
2692	042 ASP A 330	40.632	34.237	19.660	1.00	7.16	7	2745	N	LEU A 338	40.800	24.801	16.837	1.00	13.46	6
2693	043 ASP A 330	41.808	30.403	16.873	1.00	12.95	6	2746	CA	LEU A 338	41.340	26.036	16.033	1.00	13.02	6
2694	044 ASP A 330	42.466	29.890	19.211	1.00	11.99	6	2747	CB	LEU A 338	40.259	26.794	15.338	1.00	12.29	6
2695	045 ASP A 330	43.345	29.690	17.963	1.00	12.80	7	2748	O	LEU A 338	41.955	26.893	17.006	1.00	14.55	8
2696	046 ASP A 330	42.793	30.208	17.963	1.00	12.80	7	2749	CG1	LEU A 338	40.259	26.794	15.338	1.00	12.29	6
2697	047 ASP A 331	44.119	30.424	17.447	1.00	13.52	6	2750	CG2	LEU A 338	40.259	26.794	15.338	1.00	12.29	6
2698	048 ASP A 331	43.974	30.918	15.966	1.00	13.53	6	2751	C	LEU A 338	40.259	26.794	15.338	1.00	12.29	6
2699	049 ASP A 331	44.899	31.372	18.320	1.00	14.55	6	2752	O	LEU A 338	40.259	26.794	15.338	1.00	12.29	6
2700	050 ASP A 331	44.899	31.372	18.320	1.00	14.55	6	2753	N	VAL A 339	40.259	26.794	15.338	1.00	12.29	6
2701	051 ASP A 331	44.899	31.372	18.320	1.00	14.55	6	2754	CB	VAL A 339	40.259	26.794	15.338	1.00	12.29	6
2702	052 ASP A 331	44.899	31.372	18.320	1.00	14.55	6	2755	CG	VAL A 339	40.259	26.794	15.338	1.00	12.29	6
2703	053 ASP A 331	44.899	31.372	18.320	1.00	14.55	6	2756	CG1	VAL A 339	40.259	26.794	15.338	1.00	12.29	6

AT01	2757	CE2	VAL	A	339	36.745	21.811	16.483	1.00	9.265	6	AT04	2810	W	PRO	A	345	30.989	23.866	10.213	1.00	9.37	7
AT04	2758	C	VAL	A	339	38.513	23.484	13.385	1.00	12.57	6	AT04	2811	CO	PRO	A	345	31.497	24.236	8.991	1.00	9.33	6
AT04	2759	G	VAL	A	339	38.271	24.688	13.279	1.00	12.28	8	AT04	2812	CA	PRO	A	345	29.559	23.779	10.018	1.00	9.01	6
AT04	2760	H	GLH	A	340	39.016	22.686	12.404	1.00	12.55	7	AT04	2813	CB	PRO	A	345	29.285	24.245	8.592	1.00	9.17	6
AT04	2761	CA	GLH	A	340	39.288	23.502	11.088	1.00	12.55	6	AT04	2814	CB	PRO	A	345	30.576	25.008	8.288	1.00	9.42	6
AT04	2762	CB	GLH	A	340	39.975	22.357	10.097	1.00	11.11	6	AT04	2815	Q	PRO	A	345	29.077	22.331	10.309	1.00	8.68	6
AT04	2763	CG	GLH	A	340	41.372	21.974	10.559	1.00	11.55	6	AT04	2816	Q	PRO	A	345	27.992	22.162	10.862	1.00	8.28	8
AT04	2764	CO	GLH	A	340	42.073	21.105	9.513	1.00	14.34	6	AT04	2817	W	LEU	A	346	27.863	21.274	9.998	1.00	8.29	7
AT04	2765	CE1	GLH	A	340	43.594	20.802	8.384	1.00	15.11	8	AT04	2818	CA	LEU	A	346	29.491	19.890	10.274	1.00	7.82	6
AT04	2766	CE2	GLH	A	340	43.272	20.743	9.959	1.00	15.11	7	AT04	2819	CB	LEU	A	346	30.443	18.876	9.664	1.00	7.71	6
AT04	2767	C	GLH	A	340	38.009	23.900	10.468	1.00	12.34	6	AT04	2820	CG	LEU	A	346	30.608	18.730	8.147	1.00	9.48	6
AT04	2768	D	GLH	A	340	36.930	23.331	10.565	1.00	12.28	8	AT04	2821	CO1	LEU	A	346	30.910	20.053	7.472	1.00	6.38	6
AT04	2769	H	PRO	A	341	38.147	25.042	9.779	1.00	12.25	7	AT04	2822	CO2	LEU	A	346	31.710	17.710	7.794	1.00	9.58	6
AT04	2770	CA	PRO	A	341	37.026	25.753	9.200	1.00	12.38	6	AT04	2823	C	LEU	A	346	29.428	19.716	11.796	1.00	7.55	6
AT04	2771	CB	PRO	A	341	37.516	26.993	6.393	1.00	15.06	6	AT04	2824	Q	LEU	A	346	28.510	19.084	12.262	1.00	7.43	8
AT04	2772	CE1	PRO	A	341	38.100	27.874	9.353	1.00	16.92	8	AT04	2825	W	ALA	A	347	30.320	20.297	12.583	1.00	7.30	7
AT04	2773	CE2	PRO	A	341	36.347	27.684	7.716	1.00	14.77	6	AT04	2826	CA	ALA	A	347	30.425	20.274	14.019	1.00	7.11	6
AT04	2774	C	PRO	A	341	36.174	26.916	8.332	1.00	12.08	6	AT04	2827	CB	ALA	A	347	31.740	20.902	14.501	1.00	7.21	6
AT04	2775	G	PRO	A	341	34.910	25.018	8.411	1.00	12.16	8	AT04	2828	C	ALA	A	347	29.284	21.031	14.671	1.00	7.06	6
AT04	2776	H	PRO	A	342	36.698	24.095	7.465	1.00	11.85	7	AT04	2829	Q	ALA	A	347	28.712	20.958	15.670	1.00	7.03	8
AT04	2777	CA	PRO	A	342	35.902	23.225	6.585	1.00	11.19	6	AT04	2830	W	PRO	A	348	28.827	22.160	14.103	1.00	7.17	7
AT04	2778	CB	PRO	A	342	36.871	22.438	5.873	1.00	10.89	6	AT04	2831	CA	PRO	A	348	27.673	22.854	14.693	1.00	7.17	6
AT04	2779	CG	PRO	A	342	37.568	21.288	6.392	1.00	9.86	6	AT04	2832	CB	PRO	A	348	27.650	24.299	14.175	1.00	7.45	6
AT04	2780	CO2	PRO	A	342	37.073	19.949	6.491	1.00	9.37	6	AT04	2833	CG	PRO	A	348	28.510	25.236	15.008	1.00	7.77	6
AT04	2781	CE1	PRO	A	342	37.988	19.219	7.217	1.00	9.97	6	AT04	2834	CE1	PRO	A	348	29.718	25.772	14.609	1.00	7.85	6
AT04	2782	CE2	PRO	A	342	35.916	19.290	5.991	1.00	10.12	6	AT04	2835	CE1	PRO	A	348	30.416	26.670	15.435	1.00	7.87	6
AT04	2783	CO1	PRO	A	342	38.756	21.310	7.062	1.00	10.06	6	AT04	2836	CO2	PRO	A	348	28.035	25.569	16.283	1.00	7.82	6
AT04	2784	NE1	PRO	A	342	39.027	20.080	7.592	1.00	11.11	7	AT04	2837	CE2	PRO	A	348	28.731	26.430	17.105	1.00	7.89	6
AT04	2785	C2	PRO	A	342	37.809	17.853	7.527	1.00	10.11	6	AT04	2838	CE2	PRO	A	348	29.917	26.984	16.682	1.00	7.94	6
AT04	2786	C23	PRO	A	342	35.700	17.950	6.293	1.00	9.23	6	AT04	2839	CH	PRO	A	348	30.609	27.789	17.576	1.00	7.87	8
AT04	2787	CH2	PRO	A	342	36.654	17.222	7.050	1.00	10.34	6	AT04	2840	C	PRO	A	348	26.404	22.081	14.387	1.00	7.12	6
AT04	2788	C	PRO	A	342	34.968	23.340	7.391	1.00	10.76	6	AT04	2841	O	PRO	A	348	25.461	22.059	15.193	1.00	7.03	8
AT04	2789	O	PRO	A	342	33.837	22.038	6.980	1.00	10.80	8	AT04	2842	W	ALA	A	349	26.328	21.385	13.223	1.00	6.87	7
AT04	2790	H	PRO	A	343	35.375	21.846	8.577	1.00	10.45	7	AT04	2843	CA	ALA	A	349	25.127	20.607	12.939	1.00	6.67	6
AT04	2791	CA	PRO	A	343	34.544	20.979	9.389	1.00	9.81	6	AT04	2844	CB	ALA	A	349	25.131	20.070	11.515	1.00	6.51	6
AT04	2792	CB	PRO	A	343	35.520	20.888	10.193	1.00	10.81	6	AT04	2845	C	ALA	A	349	25.054	19.497	13.978	1.00	6.62	6
AT04	2793	CG	PRO	A	343	34.841	18.880	10.796	1.00	9.94	6	AT04	2846	O	ALA	A	349	23.925	19.114	14.487	1.00	6.43	8
AT04	2794	CO1	PRO	A	343	34.561	17.786	9.989	1.00	9.97	6	AT04	2847	W	PHE	A	350	26.237	18.899	14.250	1.00	6.67	7
AT04	2795	CO2	PRO	A	343	34.466	18.875	12.117	1.00	9.30	6	AT04	2848	CA	PHE	A	350	26.268	17.814	15.320	1.00	6.81	6
AT04	2796	CE1	PRO	A	343	33.947	16.653	10.506	1.00	9.66	6	AT04	2849	CB	PHE	A	350	27.701	17.250	15.304	1.00	6.91	6
AT04	2797	CE2	PRO	A	343	33.842	17.747	12.859	1.00	10.16	6	AT04	2850	CG	PHE	A	350	27.746	15.996	16.137	1.00	9.15	6
AT04	2798	C2	PRO	A	343	33.592	16.637	11.845	1.00	10.55	6	AT04	2851	CO1	PHE	A	350	27.494	14.763	15.559	1.00	8.95	6
AT04	2799	C	PRO	A	343	33.621	21.720	10.332	1.00	9.65	6	AT04	2852	CO2	PHE	A	350	28.009	16.069	17.510	1.00	11.23	6
AT04	2800	O	PHE	A	343	32.649	21.160	10.828	1.00	9.50	6	AT04	2853	CE1	PHE	A	350	27.551	13.618	16.317	1.00	10.89	6
AT04	2801	H	LYS	A	344	33.897	23.010	10.509	1.00	9.52	7	AT04	2854	CE2	PHE	A	350	28.044	14.896	18.273	1.00	11.66	6
AT04	2802	CA	LYS	A	344	33.084	23.775	11.516	1.00	9.73	6	AT04	2855	C2	PHE	A	350	27.847	13.657	17.687	1.00	10.74	6
AT04	2803	CB	LYS	A	344	33.889	25.209	11.614	1.00	11.03	6	AT04	2856	C	PHE	A	350	25.768	18.242	16.605	1.00	6.90	6
AT04	2804	CG	LYS	A	344	33.193	25.978	12.846	1.00	11.47	6	AT04	2857	O	PHE	A	350	24.978	17.547	17.275	1.00	6.86	8
AT04	2805	CO	LYS	A	344	34.235	26.954	13.366	1.00	10.60	6	AT04	2858	H	ILE	A	351	26.217	19.408	17.102	1.00	7.14	7
AT04	2806	CE	LYS	A	344	35.068	26.281	14.670	1.00	9.19	6	AT04	2859	CA	ILE	A	351	25.736	19.797	18.637	1.00	7.28	6
AT04	2807	CE2	LYS	A	344	36.098	27.262	14.962	1.00	7.52	7	AT04	2860	CB	ILE	A	351	26.767	20.663	19.194	1.00	6.43	6
AT04	2808	C	LYS	A	344	31.573	23.696	11.384	1.00	9.62	6	AT04	2861	CE2	ILE	A	351	28.086	19.924	19.275	1.00	6.52	6
AT04	2809	O	LYS	A	344	30.838	23.428	12.371	1.00	9.63	8	AT04	2862	CG1	ILE	A	351	26.943	22.034	18.556	1.00	6.43	6

14.6

2863	CO1	11E	A	351	27.589	22.986	19.575	1.00	5.33	6	2916	CE1	11R	A	358	21.449	26.080	26.747	1.00	9.42	6
2864	C	11E	A	351	24.372	20.509	18.459	1.00	7.26	6	2917	CE2	11R	A	358	22.234	26.466	28.799	1.00	9.87	6
2865	O	11E	A	351	23.668	20.349	19.408	1.00	7.46	8	2918	CE2	11R	A	358	21.900	25.783	29.085	1.00	9.55	6
2866	CA	11E	A	352	23.960	21.213	17.423	1.00	7.13	7	2919	CE2	11R	A	358	21.466	26.587	28.050	1.00	9.41	6
2867	CA	11E	A	352	22.678	21.931	17.500	1.00	7.51	6	2920	CE2	11R	A	358	21.076	27.879	28.304	1.00	8.90	8
2868	CB	11E	A	352	22.778	23.170	16.614	1.00	6.11	6	2921	C	11R	A	358	26.062	22.642	25.113	1.00	9.49	6
2869	CG	11E	A	352	23.769	24.248	17.000	1.00	7.70	6	2922	D	11R	A	358	25.195	22.737	23.552	1.00	9.20	8
2870	CO1	11E	A	352	23.973	25.292	15.878	1.00	6.26	6	2923	D	11R	A	358	23.809	22.981	23.858	1.00	9.59	7
2871	CO2	11E	A	352	23.307	24.932	18.273	1.00	6.10	6	2924	CO	11R	A	359	22.503	22.784	23.286	1.00	9.74	6
2872	C	11E	A	352	21.377	21.209	17.097	1.00	7.69	6	2925	CA	11R	A	359	24.786	23.481	22.987	1.00	9.51	6
2873	O	11E	A	352	20.314	21.666	17.512	1.00	7.18	8	2926	CB	11R	A	359	26.269	23.201	21.495	1.00	9.51	6
2874	N	11R	A	353	21.530	20.143	18.291	1.00	8.22	7	2927	CG	11R	A	359	22.763	23.211	21.778	1.00	9.71	6
2875	CA	11R	A	353	20.364	19.372	15.781	1.00	9.02	6	2928	C	11R	A	359	23.173	24.945	23.045	1.00	9.55	6
2876	CB	11R	A	353	20.420	19.145	14.234	1.00	9.08	6	2929	C	11R	A	359	26.454	25.242	22.837	1.00	9.58	7
2877	CO1	11R	A	353	21.434	18.262	13.784	1.00	8.55	8	2930	N	11R	A	360	26.454	25.242	22.837	1.00	9.58	7
2878	CO2	11R	A	353	20.559	20.504	13.543	1.00	9.72	6	2931	CA	11R	A	360	26.978	26.588	22.983	1.00	9.76	6
2879	C	11R	A	353	20.161	18.030	16.481	1.00	9.71	6	2932	CB	11R	A	360	28.115	26.640	24.024	1.00	11.01	6
2880	O	11R	A	353	19.066	17.453	16.250	1.00	9.88	8	2933	CG	11R	A	360	28.777	28.065	24.057	1.00	13.99	6
2881	N	11R	A	354	21.088	17.681	17.369	1.00	10.05	7	2934	CB	11R	A	360	30.282	28.033	24.332	1.00	15.99	6
2882	CA	11R	A	354	20.883	16.530	18.085	1.00	10.58	6	2935	CG	11R	A	360	30.427	27.709	25.524	1.00	14.42	8
2883	CB	11R	A	354	22.258	15.688	18.208	1.00	9.90	6	2936	HE2	11R	A	360	31.291	28.336	23.425	1.00	15.78	7
2884	CB	11R	A	354	22.706	15.117	16.879	1.00	8.76	6	2937	C	11R	A	360	27.481	27.096	21.007	1.00	9.39	6
2885	CO	11R	A	354	24.107	14.517	17.011	1.00	9.60	6	2938	O	11R	A	360	28.228	26.305	21.007	1.00	9.32	8
2886	HE	11R	A	354	24.016	13.348	17.864	1.00	8.67	7	2939	N	11R	A	361	27.111	28.317	21.278	1.00	9.24	7
2887	CO	11R	A	354	23.434	12.222	17.541	1.00	9.03	6	2940	CA	11R	A	361	27.586	28.925	20.032	1.00	9.26	6
2888	HE1	11R	A	354	23.392	11.309	18.513	1.00	10.30	7	2941	CB	11R	A	361	26.532	29.709	19.230	1.00	10.17	6
2889	HE2	11R	A	354	22.866	11.890	16.408	1.00	8.32	7	2942	CG	11R	A	361	27.159	30.437	18.039	1.00	9.02	6
2890	O	11R	A	354	20.103	16.563	19.378	1.00	11.10	6	2943	CG	11R	A	361	25.394	28.761	18.785	1.00	9.34	6
2891	O	11R	A	354	20.157	17.713	19.854	1.00	11.27	8	2944	C	11R	A	361	28.739	29.800	20.354	1.00	9.12	6
2892	N	11R	A	355	19.325	15.618	19.921	1.00	11.22	7	2945	C	11R	A	361	28.526	30.595	20.354	1.00	9.34	8
2893	CA	11R	A	355	18.560	15.818	21.130	1.00	11.41	6	2946	N	11R	A	362	29.879	29.687	19.703	1.00	8.60	7
2894	CB	11R	A	355	17.527	14.651	21.351	1.00	14.92	6	2947	CA	11R	A	362	30.985	30.768	20.056	1.00	8.23	6
2895	CG	11R	A	355	18.229	13.320	21.567	1.00	17.30	6	2948	CB	11R	A	362	31.606	30.771	20.058	1.00	6.40	6
2896	CO	11R	A	355	17.370	12.087	21.464	1.00	19.96	6	2949	CG	11R	A	362	33.778	31.642	21.142	1.00	5.78	6
2897	CO1	11R	A	355	17.828	10.936	21.981	1.00	21.87	6	2950	CG	11R	A	362	34.710	30.563	19.197	1.00	5.00	6
2898	CO2	11R	A	355	16.145	12.138	21.394	1.00	22.12	8	2951	CO2	11R	A	362	34.961	32.330	21.423	1.00	5.15	6
2899	O	11R	A	355	19.317	15.808	22.469	1.00	11.55	6	2952	CE1	11R	A	362	35.912	31.228	19.464	1.00	5.23	6
2900	O	11R	A	355	18.718	16.405	23.451	1.00	11.55	8	2953	CE2	11R	A	362	36.039	32.080	20.579	1.00	5.49	6
2901	N	11R	A	356	20.569	15.450	22.576	1.00	11.55	7	2954	CE2	11R	A	362	30.967	32.053	19.231	1.00	8.28	6
2902	CA	11R	A	356	21.398	14.171	24.475	1.00	13.61	6	2955	C	11R	A	362	30.857	32.004	18.043	1.00	7.85	8
2903	CB	11R	A	356	22.246	13.514	23.352	1.00	18.62	6	2956	O	11R	A	362	31.117	33.210	19.872	1.00	8.47	7
2904	CG	11R	A	356	22.241	16.607	23.975	1.00	11.33	6	2957	N	11R	A	363	31.144	34.545	19.289	1.00	8.84	6
2905	C	11R	A	356	22.863	16.940	22.971	1.00	11.70	8	2958	CA	11R	A	363	31.530	35.652	20.344	1.00	9.13	6
2906	O	11R	A	356	22.428	17.219	25.136	1.00	10.87	7	2959	CB	11R	A	363	31.530	37.081	19.976	1.00	9.86	6
2907	N	11R	A	357	23.363	18.269	25.422	1.00	10.39	6	2960	CG	11R	A	363	30.479	37.981	20.213	1.00	10.09	6
2908	CA	11R	A	357	22.619	19.622	25.239	1.00	10.36	6	2961	CO1	11R	A	363	32.585	39.317	19.904	1.00	10.35	6
2909	O	11R	A	357	21.602	19.837	24.547	1.00	10.17	8	2962	CO1	11R	A	363	32.709	37.609	19.410	1.00	10.25	6
2910	O	11R	A	357	23.253	20.608	25.800	1.00	10.01	7	2963	CO2	11R	A	363	32.850	38.956	19.091	1.00	10.30	6
2911	N	11R	A	358	22.884	22.017	25.877	1.00	9.76	6	2964	CE2	11R	A	363	31.776	39.774	19.365	1.00	10.78	6
2912	CA	11R	A	358	22.689	22.698	27.311	1.00	9.68	6	2965	CE2	11R	A	363	31.811	41.126	19.087	1.00	11.58	8
2913	CB	11R	A	358	23.268	23.937	27.516	1.00	9.61	6	2966	CO	11R	A	363	32.241	34.680	18.187	1.00	8.73	6
2914	CG	11R	A	358	21.829	24.775	26.494	1.00	9.48	6	2967	C	11R	A	363	32.011	35.363	17.191	1.00	8.42	8
2915	CO1	11R	A	358							2968	O	11R	A	363						

SUBSTITUTE SHEET (RULE 26)

A104	2670	H	GLY A 364	33.399	34.040	18.452	1.00	8.36	7	A104	3022	CA	GLY A 371	43.889	37.991	16.742	1.00	22.15	6
A104	2670	CA	GLY A 364	34.472	34.061	17.503	1.00	8.81	6	A104	3023	C	GLY A 371	44.817	38.443	15.581	1.00	23.36	6
A104	2671	C	GLY A 364	34.683	33.281	18.231	1.00	9.84	6	A104	3024	O	GLY A 371	44.393	38.896	14.521	1.00	23.05	8
A104	2672	O	GLY A 364	34.596	31.639	15.156	1.00	8.91	8	A104	3025	H	ASP A 372	46.095	38.233	15.877	1.00	24.83	7
A104	2673	H	ASP A 365	33.233	32.251	16.337	1.00	9.21	7	A104	3026	CA	ASP A 372	47.186	38.626	15.016	1.00	24.55	6
A104	2674	CA	ASP A 365	32.830	31.513	15.137	1.00	9.93	6	A104	3027	CB	ASP A 372	48.323	39.306	15.874	1.00	31.39	6
A104	2675	CB	ASP A 365	32.255	30.146	15.429	1.00	8.93	6	A104	3028	CG	ASP A 372	47.982	40.791	15.968	1.00	34.93	6
A104	2676	CG	ASP A 365	33.349	29.235	15.977	1.00	9.58	8	A104	3029	OO1	ASP A 372	47.609	41.363	14.906	1.00	37.36	8
A104	2677	OO2	ASP A 365	34.516	29.422	15.641	1.00	10.56	8	A104	3030	OO2	ASP A 372	47.972	41.443	17.034	1.00	37.47	8
A104	2678	OO2	ASP A 365	33.078	28.275	16.700	1.00	9.75	8	A104	3031	C	ASP A 372	47.796	37.528	14.189	1.00	27.31	6
A104	2679	C	ASP A 365	31.780	32.266	14.321	1.00	10.69	6	A104	3032	H	SEB A 373	48.870	37.818	13.613	1.00	27.66	7
A104	2680	O	ASP A 365	31.770	32.135	13.078	1.00	10.75	8	A104	3033	H	SEB A 373	47.162	36.353	14.146	1.00	27.66	7
A104	2681	H	HE1 A 366	30.887	32.996	14.980	1.00	11.30	7	A104	3034	CA	SEB A 373	47.800	35.318	13.305	1.00	27.95	6
A104	2682	CA	HE1 A 366	29.657	33.792	14.293	1.00	11.93	8	A104	3035	CB	SEB A 373	47.478	33.986	13.932	1.00	24.91	6
A104	2683	CB	HE1 A 366	28.638	34.351	15.103	1.00	14.14	6	A104	3036	CG	SEB A 373	46.393	33.436	13.642	1.00	28.21	8
A104	2684	CG	HE1 A 366	27.828	33.348	15.827	1.00	17.97	6	A104	3037	C	SEB A 373	47.255	35.373	11.873	1.00	28.21	8
A104	2685	SO	HE1 A 366	26.475	33.032	14.646	1.00	22.02	16	A104	3038	O	SEB A 373	46.480	36.189	11.346	1.00	28.10	8
A104	2686	CE	HE1 A 366	25.576	34.590	14.752	1.00	20.81	6	A104	3039	H	GLH A 374	47.780	34.393	11.137	1.00	28.61	7
A104	2687	C	HE1 A 366	30.455	35.016	13.604	1.00	12.33	6	A104	3040	CA	GLH A 374	47.348	34.201	9.729	1.00	28.86	6
A104	2688	O	HE1 A 366	30.240	35.367	12.425	1.00	12.31	7	A104	3041	CB	GLH A 374	48.525	34.112	8.767	1.00	34.24	6
A104	2689	H	HE1 A 367	31.249	35.740	14.417	1.00	12.74	7	A104	3042	CG	GLH A 374	49.400	35.309	8.530	1.00	40.44	6
A104	2690	CA	HE1 A 367	31.831	36.966	13.927	1.00	13.46	6	A104	3043	CG	GLH A 374	48.939	36.714	8.874	1.00	45.21	6
A104	2691	CB	HE1 A 367	31.540	38.065	14.988	1.00	14.31	6	A104	3044	OE1	GLH A 374	48.111	37.342	8.149	1.00	47.86	8
A104	2692	CG	HE1 A 367	30.092	38.282	15.374	1.00	15.58	6	A104	3045	OE2	GLH A 374	49.449	37.277	10.005	1.00	45.97	7
A104	2693	CO1	HE1 A 367	29.721	38.284	16.730	1.00	15.98	6	A104	3046	C	GLH A 374	46.414	32.963	9.719	1.00	28.21	6
A104	2694	CE1	HE1 A 367	28.040	38.438	17.141	1.00	16.47	6	A104	3047	H	ARG A 375	45.952	32.517	8.674	1.00	28.76	8
A104	2695	CO2	HE1 A 367	29.075	38.425	16.433	1.00	16.06	6	A104	3048	O	ARG A 375	45.952	32.517	10.873	1.00	26.96	7
A104	2696	CE2	HE1 A 367	27.776	38.629	16.845	1.00	16.69	6	A104	3049	CA	ARG A 375	45.064	31.421	11.109	1.00	25.60	6
A104	2697	CE	HE1 A 367	27.431	38.644	16.196	1.00	16.89	6	A104	3050	CB	ARG A 375	45.641	30.394	12.115	1.00	29.84	6
A104	2698	OH	HE1 A 367	26.105	38.815	16.533	1.00	16.92	6	A104	3051	CG	ARG A 375	46.842	29.713	11.509	1.00	33.75	6
A104	2699	C	HE1 A 367	33.299	36.913	13.589	1.00	13.51	6	A104	3052	CG	ARG A 375	48.088	29.365	12.067	1.00	36.33	6
A104	3001	H	GLY A 368	34.050	35.837	13.717	1.00	13.66	7	A104	3053	HE	ARG A 375	47.016	28.308	13.998	1.00	37.77	7
A104	3002	CA	GLY A 368	35.472	35.957	13.348	1.00	14.18	6	A104	3054	C2	ARG A 375	47.854	29.261	14.351	1.00	37.09	6
A104	3003	C	GLY A 368	36.289	36.369	14.599	1.00	14.83	6	A104	3055	WH1	ARG A 375	48.293	29.399	15.587	1.00	36.83	7
A104	3004	O	GLY A 368	35.745	36.992	15.528	1.00	15.20	8	A104	3056	WH2	ARG A 375	43.777	31.845	11.827	1.00	23.88	6
A104	3005	H	HE1 A 369	37.531	35.971	14.691	1.00	14.98	7	A104	3057	C	ARG A 375	43.218	30.942	12.450	1.00	23.81	8
A104	3006	CA	HE1 A 369	38.409	36.330	15.759	1.00	15.75	6	A104	3058	O	ARG A 375	42.196	33.558	12.450	1.00	20.37	6
A104	3007	CB	HE1 A 369	39.185	35.126	16.318	1.00	14.08	6	A104	3059	H	GLU A 376	42.061	35.088	12.418	1.00	17.56	6
A104	3008	OG1	HE1 A 369	39.926	34.392	15.324	1.00	11.76	8	A104	3060	CA	GLU A 376	43.399	33.116	11.777	1.00	22.28	7
A104	3009	CG2	HE1 A 369	38.175	34.186	16.966	1.00	10.90	6	A104	3061	CB	GLU A 376	42.061	35.088	12.418	1.00	16.13	6
A104	3010	C	HE1 A 369	39.346	37.437	15.225	1.00	16.84	6	A104	3062	CG	GLU A 376	43.203	35.780	13.151	1.00	14.90	6
A104	3011	O	HE1 A 369	39.727	37.643	16.039	1.00	16.53	8	A104	3063	CO	GLU A 376	43.361	35.421	14.595	1.00	14.90	6
A104	3012	H	LVS A 370	39.733	38.369	16.190	1.00	17.86	7	A104	3064	OE1	GLU A 376	42.403	35.436	15.391	1.00	12.95	8
A104	3013	CA	LVS A 370	40.568	39.488	15.712	1.00	19.16	6	A104	3065	OE2	GLU A 376	44.510	35.188	15.051	1.00	16.10	8
A104	3014	CB	LVS A 370	39.849	40.792	16.131	1.00	22.20	6	A104	3066	C	GLU A 376	40.955	32.886	13.869	1.00	19.17	6
A104	3015	CG	LVS A 370	38.702	41.073	15.133	1.00	26.42	6	A104	3067	O	GLU A 376	40.801	32.503	10.715	1.00	18.94	8
A104	3016	CO	LVS A 370	39.254	41.271	13.736	1.00	29.66	6	A104	3068	H	LLE A 377	40.002	32.698	12.777	1.00	18.23	7
A104	3017	CE	LVS A 370	38.356	41.239	12.544	1.00	32.10	6	A104	3069	CA	LLE A 377	38.726	32.102	12.410	1.00	17.23	6
A104	3018	HE	LVS A 370	39.111	41.178	11.243	1.00	31.93	7	A104	3070	CB	LLE A 377	37.924	31.634	13.636	1.00	15.28	6
A104	3019	C	LVS A 370	41.998	39.642	16.214	1.00	19.90	8	A104	3071	CG2	LLE A 377	36.616	30.961	13.205	1.00	15.23	6
A104	3020	O	LVS A 370	42.638	40.436	16.526	1.00	19.78	6	A104	3072	CG1	LLE A 377	38.720	30.715	14.564	1.00	14.23	6
A104	3021	H	GLY A 371	42.534	39.244	16.359	1.00	20.85	7	A104	3073	CO1	LLE A 377	38.109	30.512	15.935	1.00	13.53	6
A104	3022	N	GLY A 371	42.534	39.244	16.359	1.00	20.85	7	A104	3074	C	LLE A 377	37.957	33.184	11.860	1.00	18.78	6

ATOM	3075	O	ILE A 377	37,783	34,301	12,173	1,00	16,90	8	ATOM	3128	CG1	ILE A 384	28,029	28,790	12,411	1,00	13,78	6
ATOM	3076	N	PRO A 378	37,451	32,927	10,461	1,00	16,21	7	ATOM	3129	CB1	ILE A 384	28,903	29,649	13,343	1,00	13,12	6
ATOM	3077	CO	PRO A 378	37,634	31,617	9,821	1,00	16,80	6	ATOM	3130	C	ILE A 384	24,335	29,241	11,430	1,00	12,81	8
ATOM	3078	EA	PRO A 378	36,637	33,810	9,495	1,00	15,87	6	ATOM	3131	O	ILE A 384	23,621	28,363	11,931	1,00	12,68	8
ATOM	3079	CB	PRO A 378	36,553	33,232	8,283	1,00	15,98	6	ATOM	3132	N	GLU A 385	23,841	30,401	11,025	1,00	12,22	7
ATOM	3080	CG	PRO A 378	37,023	31,835	8,456	1,00	15,94	6	ATOM	3133	CA	GLU A 385	22,459	30,804	11,178	1,00	12,09	6
ATOM	3081	C	PRO A 378	35,214	33,860	10,247	1,00	15,56	6	ATOM	3134	CB	GLU A 385	22,249	32,252	10,471	1,00	13,25	6
ATOM	3082	O	PRO A 378	34,741	32,945	10,946	1,00	15,55	6	ATOM	3135	CG	GLU A 385	23,039	33,148	11,637	1,00	16,06	6
ATOM	3083	N	ALA A 379	34,506	34,960	9,931	1,00	15,19	7	ATOM	3136	CD	GLU A 385	22,881	34,621	11,531	1,00	18,04	6
ATOM	3084	CA	ALA A 379	33,093	35,063	10,370	1,00	14,83	6	ATOM	3137	OE1	GLU A 385	22,082	35,050	10,531	1,00	18,27	8
ATOM	3085	CB	ALA A 379	32,523	36,450	10,119	1,00	13,37	6	ATOM	3138	OE2	GLU A 385	22,960	35,427	12,453	1,00	18,60	8
ATOM	3086	C	ALA A 379	32,246	33,979	9,679	1,00	14,60	6	ATOM	3139	C	GLU A 385	21,439	29,867	10,367	1,00	11,96	6
ATOM	3087	O	ALA A 379	32,082	33,990	8,438	1,00	14,65	8	ATOM	3140	O	GLU A 385	20,439	29,688	11,273	1,00	12,04	8
ATOM	3088	N	LEU A 380	31,703	33,021	10,428	1,00	14,28	7	ATOM	3141	N	PRO A 386	21,814	29,238	9,436	1,00	11,74	7
ATOM	3089	CA	LEU A 380	30,935	31,960	9,792	1,00	14,14	6	ATOM	3142	CD	PRO A 386	22,735	29,467	8,528	1,00	11,74	6
ATOM	3090	CB	LEU A 380	31,468	30,817	10,265	1,00	15,00	6	ATOM	3143	CA	PRO A 386	20,676	28,265	8,905	1,00	11,52	6
ATOM	3091	CG	LEU A 380	32,913	30,303	9,865	1,00	18,56	6	ATOM	3144	CB	PRO A 386	21,205	27,847	7,316	1,00	11,54	6
ATOM	3092	CD1	LEU A 380	32,975	30,004	8,350	1,00	16,26	6	ATOM	3145	CG	PRO A 386	22,167	28,967	7,199	1,00	11,74	6
ATOM	3093	CD2	LEU A 380	28,602	31,262	9,773	1,00	14,38	8	ATOM	3146	C	PRO A 386	20,545	27,050	9,826	1,00	11,28	6
ATOM	3094	C	LEU A 380	29,448	32,123	10,017	1,00	14,34	6	ATOM	3147	O	PRO A 386	19,493	26,419	9,863	1,00	11,21	8
ATOM	3095	O	LEU A 380	27,811	31,278	10,475	1,00	14,34	7	ATOM	3148	N	ILE A 387	21,617	26,648	10,510	1,00	11,05	7
ATOM	3096	CA	LYS A 381	27,615	33,579	10,719	1,00	14,84	6	ATOM	3149	CA	ILE A 387	21,619	25,492	11,424	1,00	10,84	6
ATOM	3097	CB	LYS A 381	27,672	35,101	10,830	1,00	10,02	6	ATOM	3150	CB	ILE A 387	23,647	24,957	11,653	1,00	8,79	6
ATOM	3098	CG	LYS A 381	26,382	35,855	10,702	1,00	21,47	6	ATOM	3151	CD2	ILE A 387	22,978	23,619	12,340	1,00	8,90	6
ATOM	3099	CG	LYS A 381	26,754	37,314	10,944	1,00	25,20	6	ATOM	3152	CD1	ILE A 387	23,799	24,850	10,310	1,00	8,27	6
ATOM	3100	CO	LYS A 381	25,912	38,275	10,104	1,00	28,61	6	ATOM	3153	CD1	ILE A 387	25,231	24,430	10,511	1,00	9,38	6
ATOM	3101	CE	LYS A 381	25,564	38,411	10,770	1,00	30,73	7	ATOM	3154	C	ILE A 387	20,917	25,608	12,754	1,00	11,01	6
ATOM	3102	N2	LYS A 381	26,467	33,104	9,434	1,00	14,98	6	ATOM	3155	O	ILE A 387	20,273	24,946	13,366	1,00	10,92	8
ATOM	3103	C	LYS A 381	25,589	32,577	9,911	1,00	14,84	8	ATOM	3156	N	LEU A 388	21,058	27,064	13,176	1,00	11,09	7
ATOM	3104	O	LYS A 381	26,978	33,273	8,350	1,00	14,98	7	ATOM	3157	CA	LEU A 388	20,400	27,620	14,345	1,00	11,19	6
ATOM	3105	N	ILE A 382	26,079	32,889	7,268	1,00	15,72	6	ATOM	3158	CB	LEU A 388	22,902	29,010	14,682	1,00	10,46	6
ATOM	3106	CA	ILE A 382	26,562	33,593	5,986	1,00	21,24	6	ATOM	3159	CO	LEU A 388	22,084	29,061	15,638	1,00	11,84	6
ATOM	3107	CB	ILE A 382	28,036	33,424	5,842	1,00	25,72	6	ATOM	3160	CD1	LEU A 388	22,502	30,545	15,745	1,00	11,69	6
ATOM	3108	CG	ILE A 382	29,070	33,878	6,415	1,00	27,36	6	ATOM	3161	CD2	LEU A 388	21,636	28,377	16,916	1,00	10,70	6
ATOM	3109	CD2	ILE A 382	28,569	32,671	4,810	1,00	20,03	7	ATOM	3162	C	LEU A 388	18,887	27,688	16,042	1,00	11,21	6
ATOM	3110	HD1	ILE A 382	30,216	33,424	6,041	1,00	28,60	7	ATOM	3163	O	LEU A 388	18,017	27,443	14,899	1,00	11,36	8
ATOM	3111	HE1	ILE A 382	25,947	31,415	7,118	1,00	15,05	6	ATOM	3164	N	LYS A 389	18,551	28,015	12,792	1,00	11,22	7
ATOM	3112	HE2	ILE A 382	26,887	30,595	7,632	1,00	14,81	7	ATOM	3165	CA	LYS A 389	17,162	28,017	12,353	1,00	11,08	6
ATOM	3113	C	ILE A 382	26,002	29,161	7,135	1,00	14,36	6	ATOM	3166	CB	LYS A 389	17,016	28,533	10,952	1,00	14,65	6
ATOM	3114	O	ILE A 382	29,014	29,301	6,505	1,00	20,51	6	ATOM	3167	CG	LYS A 389	15,591	28,645	10,402	1,00	20,09	6
ATOM	3115	N	LYS A 383	28,168	28,551	7,528	1,00	14,14	6	ATOM	3168	CD	LYS A 389	15,454	30,134	9,985	1,00	24,31	6
ATOM	3116	CA	LYS A 383	29,147	28,507	5,230	1,00	23,48	6	ATOM	3169	CE	LYS A 389	14,800	30,232	8,592	1,00	27,30	6
ATOM	3117	CB	LYS A 383	30,673	28,550	4,977	1,00	26,50	6	ATOM	3170	N2	LYS A 389	13,449	29,317	8,568	1,00	30,42	7
ATOM	3118	CG	LYS A 383	31,046	29,207	3,792	1,00	27,91	7	ATOM	3171	C	LYS A 389	16,620	26,568	12,317	1,00	10,52	6
ATOM	3119	CD	LYS A 383	26,207	28,595	8,926	1,00	13,68	6	ATOM	3172	O	LYS A 389	15,474	26,308	12,746	1,00	10,45	8
ATOM	3120	CE	LYS A 383	26,207	28,595	8,926	1,00	13,68	6	ATOM	3173	N	ALA A 390	17,445	25,613	11,937	1,00	10,03	7
ATOM	3121	N2	LYS A 393	26,207	28,595	8,926	1,00	13,68	6	ATOM	3174	CA	ALA A 390	17,007	24,226	12,828	1,00	9,88	4
ATOM	3122	C	LYS A 383	26,207	28,595	8,926	1,00	13,68	6	ATOM	3175	CB	ALA A 390	17,970	23,263	11,375	1,00	7,86	6
ATOM	3123	O	LYS A 383	26,207	28,595	8,926	1,00	13,68	6	ATOM	3176	C	ALA A 390	16,868	23,832	13,506	1,00	9,86	6
ATOM	3124	N	ILE A 384	26,351	29,374	10,004	1,00	13,23	7	ATOM	3177	D	ALA A 390	15,876	23,103	13,161	1,00	9,92	8
ATOM	3125	CA	ILE A 384	25,814	28,689	11,652	1,00	12,99	6	ATOM	3178	N	ARG A 391	17,713	24,258	14,440	1,00	9,66	7
ATOM	3126	CB	ILE A 384	26,009	29,381	12,486	1,00	13,25	6	ATOM	3179	CA	ARG A 391	17,540	23,914	15,857	1,00	9,64	6
ATOM	3127	CG2	ILE A 384	25,905	29,000	13,778	1,00	12,19	6	ATOM	3180	CB	ARG A 391	18,666	24,410	16,800	1,00	8,27	6

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ATOM	3181	CB	ARG A 391	18.295	24.255	18.295	1.00	6.17	6	ATOM	3234	C	TIR A 396	11.624	16.631	17.499	1.00	10.90	6
ATOM	3182	CD	ARG A 391	19.637	24.301	19.679	1.00	6.11	6	ATOM	3235	D	TIR A 396	11.615	16.137	16.372	1.00	10.58	6
ATOM	3183	RE	ARG A 391	19.415	23.982	20.474	1.00	6.39	7	ATOM	3236	N	GLY A 397	11.252	15.899	18.553	1.00	11.07	7
ATOM	3184	CZ	ARG A 391	19.431	22.752	21.057	1.00	8.41	6	ATOM	3237	CA	GLY A 397	10.772	14.542	18.296	1.00	11.32	6
ATOM	3185	RH1	ARG A 391	19.871	21.719	20.864	1.00	7.01	7	ATOM	3238	C	GLY A 397	11.808	13.650	18.353	1.00	11.58	6
ATOM	3186	RH2	ARG A 391	19.147	22.533	22.359	1.00	6.75	7	ATOM	3239	D	GLY A 397	13.001	13.761	18.466	1.00	12.00	8
ATOM	3187	C	ARG A 391	16.258	24.518	16.534	1.00	9.84	6	ATOM	3240	N	ALA A 398	11.341	12.228	18.304	1.00	11.57	7
ATOM	3188	D	ARG A 391	16.462	23.860	17.089	1.00	9.35	8	ATOM	3241	CA	ALA A 398	12.172	11.844	18.341	1.00	11.80	6
ATOM	3189	N	LYS A 392	15.061	25.811	16.184	1.00	10.42	7	ATOM	3242	CB	ALA A 398	13.261	9.824	18.105	1.00	9.85	6
ATOM	3190	CA	LYS A 392	16.904	26.555	16.666	1.00	11.31	6	ATOM	3243	C	ALA A 398	13.348	11.115	17.365	1.00	12.04	6
ATOM	3191	CB	LYS A 392	15.137	28.036	16.253	1.00	13.27	6	ATOM	3244	D	ALA A 398	13.259	11.647	18.176	1.00	12.09	8
ATOM	3192	CE	LYS A 392	14.066	28.928	16.797	1.00	16.07	6	ATOM	3245	N	GLM A 399	16.532	10.788	17.833	1.00	12.00	7
ATOM	3193	CD	LYS A 392	14.176	30.388	16.369	1.00	20.09	6	ATOM	3246	CA	GLM A 399	15.761	10.691	17.058	1.00	12.04	6
ATOM	3194	DE	LYS A 392	12.806	31.069	16.665	1.00	26.05	7	ATOM	3247	CB	GLM A 399	16.871	11.357	17.912	1.00	10.48	6
ATOM	3195	RZ	LYS A 392	12.989	32.560	16.682	1.00	26.05	7	ATOM	3248	CG	GLM A 399	18.261	11.287	17.346	1.00	9.54	6
ATOM	3196	C	LYS A 392	13.536	26.046	16.200	1.00	11.94	6	ATOM	3249	CG	GLM A 399	19.195	12.249	18.066	1.00	9.97	6
ATOM	3197	D	LYS A 392	12.990	25.903	17.011	1.00	11.92	8	ATOM	3250	CE1	GLM A 399	18.983	13.467	18.191	1.00	8.29	8
ATOM	3198	N	GLM A 393	13.349	25.676	14.916	1.00	12.38	7	ATOM	3251	HE2	GLM A 399	20.368	11.751	18.528	1.00	9.30	7
ATOM	3199	CA	GLM A 393	12.991	25.218	14.386	1.00	12.80	6	ATOM	3252	C	GLM A 399	16.212	9.307	16.443	1.00	12.27	6
ATOM	3200	CB	GLM A 393	11.736	25.967	13.069	1.00	17.13	6	ATOM	3253	D	GLM A 399	16.158	8.327	17.361	1.00	12.29	8
ATOM	3201	CG	GLM A 393	12.463	27.237	12.917	1.00	29.33	6	ATOM	3254	N	GLM A 400	17.270	7.893	14.903	1.00	12.28	6
ATOM	3202	CD	GLM A 393	11.701	28.402	12.516	1.00	29.33	6	ATOM	3255	CA	HIS A 400	16.419	7.243	13.800	1.00	12.34	6
ATOM	3203	DE1	GLM A 393	10.856	29.003	13.159	1.00	31.70	7	ATOM	3256	CB	HIS A 400	15.001	6.998	14.252	1.00	13.76	6
ATOM	3204	HE2	GLM A 393	11.921	23.764	13.940	1.00	12.57	6	ATOM	3257	CG	HIS A 400	14.464	6.087	15.135	1.00	12.53	6
ATOM	3205	C	GLM A 393	10.718	23.422	13.819	1.00	12.77	8	ATOM	3258	CD2	HIS A 400	13.959	7.856	13.831	1.00	13.34	7
ATOM	3206	D	GLM A 394	12.839	21.690	13.678	1.00	11.99	7	ATOM	3259	HD1	HIS A 400	12.860	7.408	14.435	1.00	11.97	6
ATOM	3208	CA	TIR A 394	13.577	21.661	11.798	1.00	11.56	6	ATOM	3261	HE2	HIS A 400	13.093	6.378	15.194	1.00	11.69	7
ATOM	3209	CB	TIR A 394	12.942	22.687	10.852	1.00	12.27	6	ATOM	3262	C	HIS A 400	18.710	8.179	14.411	1.00	12.21	6
ATOM	3210	CD	TIR A 394	13.444	23.941	10.588	1.00	12.30	6	ATOM	3263	D	HIS A 400	18.909	9.132	13.670	1.00	11.78	8
ATOM	3211	CD1	TIR A 394	12.811	24.826	9.747	1.00	12.61	6	ATOM	3264	N	ASP A 401	19.651	7.332	14.895	1.00	12.31	7
ATOM	3212	CD2	TIR A 394	11.754	22.328	10.236	1.00	12.73	6	ATOM	3265	CA	ASP A 401	21.043	7.503	14.536	1.00	12.71	6
ATOM	3214	CE2	TIR A 394	11.066	23.192	9.378	1.00	13.02	6	ATOM	3266	CB	ASP A 401	21.964	7.308	15.758	1.00	15.32	6
ATOM	3215	CE	TIR A 394	11.615	24.442	9.136	1.00	13.05	6	ATOM	3267	CG	ASP A 401	21.883	8.427	16.767	1.00	18.10	6
ATOM	3216	DH	TIR A 394	10.942	25.224	8.229	1.00	13.25	8	ATOM	3268	CD1	ASP A 401	21.438	9.578	16.520	1.00	20.24	8
ATOM	3217	C	TIR A 394	13.360	20.552	14.017	1.00	11.27	6	ATOM	3269	CD2	ASP A 401	22.299	8.187	17.921	1.00	19.29	8
ATOM	3218	D	TIR A 394	12.866	19.424	13.834	1.00	10.94	8	ATOM	3270	C	ASP A 401	21.556	6.515	13.484	1.00	12.57	6
ATOM	3219	N	ALA A 395	14.338	20.794	14.988	1.00	10.88	7	ATOM	3271	D	ASP A 401	21.145	5.360	13.403	1.00	12.31	8
ATOM	3220	CA	ALA A 395	14.896	19.692	15.694	1.00	10.74	6	ATOM	3272	N	TIR A 402	22.383	8.972	12.584	1.00	12.55	7
ATOM	3221	CB	ALA A 395	16.105	20.151	16.074	1.00	8.72	6	ATOM	3273	CA	TIR A 402	22.977	6.173	11.524	1.00	12.83	6
ATOM	3222	C	ALA A 395	14.101	19.267	16.928	1.00	10.85	6	ATOM	3274	CB	TIR A 402	22.385	6.495	10.138	1.00	12.98	6
ATOM	3223	D	ALA A 395	16.102	19.591	18.063	1.00	10.94	8	ATOM	3275	CG	TIR A 402	20.891	6.179	10.103	1.00	12.98	6
ATOM	3224	N	TIR A 396	12.986	18.545	16.743	1.00	10.85	7	ATOM	3276	CD1	TIR A 402	19.990	7.186	10.479	1.00	13.23	6
ATOM	3225	CA	TIR A 396	12.061	18.070	17.753	1.00	10.80	6	ATOM	3277	CE1	TIR A 402	18.631	6.952	10.544	1.00	13.54	6
ATOM	3226	CB	TIR A 396	10.763	18.949	17.821	1.00	10.80	6	ATOM	3278	CD2	TIR A 402	20.378	4.927	9.801	1.00	13.10	6
ATOM	3227	CG	TIR A 396	11.083	20.390	18.180	1.00	10.52	6	ATOM	3279	CE2	TIR A 402	19.018	4.654	9.819	1.00	13.39	6
ATOM	3228	CD1	TIR A 396	11.233	21.365	17.195	1.00	10.23	6	ATOM	3280	CE3	TIR A 402	18.168	5.676	10.195	1.00	14.02	6
ATOM	3229	CE1	TIR A 396	11.683	22.665	17.546	1.00	10.24	6	ATOM	3281	OH	TIR A 402	16.795	5.502	10.282	1.00	14.72	8
ATOM	3230	CE2	TIR A 396	11.215	20.744	19.504	1.00	10.24	6	ATOM	3282	C	TIR A 402	24.478	6.371	11.592	1.00	13.30	6
ATOM	3231	CE2	TIR A 396	11.536	22.043	19.835	1.00	10.18	6	ATOM	3283	D	TIR A 402	25.819	7.854	10.747	1.00	13.17	8
ATOM	3232	C2	TIR A 396	11.799	22.984	18.874	1.00	10.23	6	ATOM	3284	N	PHE A 403	25.162	5.818	12.581	1.00	14.08	7
ATOM	3233	OH	TIR A 396	12.200	24.217	19.305	1.00	10.59	8	ATOM	3285	CA	PHE A 403	26.591	5.861	12.792	1.00	14.73	6
ATOM										ATOM	3286	CB	PHE A 403	26.978	6.038	14.266	1.00	16.26	6

ATOM	3287	CG	PHE	A	403	26.766	7.486	14.465	1.00	19.71	6	ATOM	3340	CA	VAL	A	409	27.012	9.436	9.309	1.00	11.68	6
ATOM	3288	CD1	PHE	A	403	25.574	7.927	15.176	1.00	20.07	6	ATOM	3341	CB	VAL	A	409	27.735	9.616	10.638	1.00	13.02	6
ATOM	3289	CD2	PHE	A	403	27.748	8.440	14.483	1.00	21.01	6	ATOM	3342	CE1	VAL	A	409	28.916	8.661	10.804	1.00	14.14	6
ATOM	3290	CE1	PHE	A	403	25.379	9.241	15.534	1.00	21.71	6	ATOM	3343	CE2	VAL	A	409	28.293	11.030	10.817	1.00	11.59	6
ATOM	3291	CE2	PHE	A	403	27.540	9.784	14.804	1.00	22.26	6	ATOM	3344	C	VAL	A	409	25.823	10.380	9.245	1.00	11.38	6
ATOM	3292	CZ	PHE	A	403	26.338	10.216	15.345	1.00	21.47	6	ATOM	3345	D	VAL	A	409	25.887	11.441	8.613	1.00	11.38	8
ATOM	3293	C	PHE	A	403	27.113	4.537	12.220	1.00	15.16	6	ATOM	3346	H	GLY	A	610	24.747	10.000	9.898	1.00	10.96	7
ATOM	3294	D	PHE	A	403	27.616	3.625	12.902	1.00	15.23	8	ATOM	3347	CA	GLY	A	610	23.548	10.842	9.910	1.00	10.41	6
ATOM	3295	H	ASP	A	404	26.987	4.370	10.906	1.00	15.33	7	ATOM	3348	C	GLY	A	610	22.635	10.508	11.084	1.00	9.89	6
ATOM	3296	CA	ASP	A	404	27.198	3.103	10.294	1.00	15.39	6	ATOM	3349	D	GLY	A	610	22.871	9.547	11.830	1.00	9.68	8
ATOM	3297	CB	ASP	A	404	26.115	2.428	9.754	1.00	17.33	6	ATOM	3350	H	TRP	A	611	21.623	11.347	11.201	1.00	9.60	7
ATOM	3298	CG	ASP	A	404	25.433	3.431	8.838	1.00	19.38	6	ATOM	3351	CA	TRP	A	611	20.569	11.201	12.204	1.00	9.34	6
ATOM	3299	CD1	ASP	A	404	25.670	4.578	8.544	1.00	19.66	8	ATOM	3352	CB	TRP	A	611	20.994	11.750	13.574	1.00	8.12	6
ATOM	3300	CD2	ASP	A	404	24.330	3.068	8.407	1.00	21.24	8	ATOM	3353	CG	TRP	A	611	21.417	13.213	13.561	1.00	8.50	6
ATOM	3301	C	ASP	A	404	28.364	3.116	9.119	1.00	15.47	6	ATOM	3354	CD2	TRP	A	611	22.726	13.662	13.285	1.00	8.48	6
ATOM	3302	O	ASP	A	404	28.339	2.154	8.320	1.00	15.71	6	ATOM	3355	CE2	TRP	A	611	22.609	15.049	13.356	1.00	8.47	6
ATOM	3303	H	HIS	A	405	29.168	4.144	8.997	1.00	15.11	7	ATOM	3356	CE3	TRP	A	611	23.924	13.810	12.971	1.00	9.18	6
ATOM	3304	CA	HIS	A	405	30.098	4.238	7.885	1.00	14.80	6	ATOM	3357	CD1	TRP	A	611	20.647	14.285	13.808	1.00	6.27	6
ATOM	3305	CB	HIS	A	405	29.332	4.913	6.719	1.00	14.80	6	ATOM	3358	CE1	TRP	A	611	21.483	15.439	13.671	1.00	6.58	7
ATOM	3306	CG	HIS	A	405	30.167	4.926	5.492	1.00	15.21	6	ATOM	3359	CE2	TRP	A	611	23.830	15.839	13.113	1.00	9.35	6
ATOM	3307	CD2	HIS	A	405	30.385	3.954	4.561	1.00	15.68	6	ATOM	3360	CE3	TRP	A	611	25.054	13.814	12.732	1.00	9.35	6
ATOM	3308	CD1	HIS	A	405	30.992	5.990	5.197	1.00	15.84	7	ATOM	3361	CE2	TRP	A	611	25.007	15.163	12.799	1.00	9.69	6
ATOM	3309	CE1	HIS	A	405	31.654	5.723	4.041	1.00	16.58	6	ATOM	3362	C	TRP	A	611	19.296	11.897	11.708	1.00	9.23	6
ATOM	3310	CE2	HIS	A	405	31.309	4.491	3.880	1.00	17.15	7	ATOM	3363	D	TRP	A	611	19.372	12.824	10.901	1.00	8.76	9
ATOM	3311	C	HIS	A	405	31.280	5.023	3.880	1.00	14.46	6	ATOM	3364	H	TRP	A	612	18.151	11.418	12.226	1.00	9.36	7
ATOM	3312	O	HIS	A	405	31.008	5.908	9.197	1.00	14.63	8	ATOM	3365	CA	TRP	A	612	16.877	12.015	11.894	1.00	9.69	6
ATOM	3313	H	HIS	A	406	32.494	4.841	7.963	1.00	14.11	7	ATOM	3366	CB	TRP	A	612	15.968	11.081	11.040	1.00	10.82	6
ATOM	3314	CA	HIS	A	406	33.630	5.587	8.495	1.00	13.78	6	ATOM	3367	CD1	TRP	A	612	15.687	9.914	11.826	1.00	12.10	8
ATOM	3315	CB	HIS	A	406	35.000	4.932	8.189	1.00	15.67	6	ATOM	3368	CE2	TRP	A	612	16.614	10.613	9.743	1.00	9.28	6
ATOM	3316	CG	HIS	A	406	34.981	4.418	6.777	1.00	16.76	6	ATOM	3369	C	TRP	A	612	16.396	12.441	13.173	1.00	9.93	6
ATOM	3317	CD2	HIS	A	406	34.505	3.285	6.232	1.00	16.51	6	ATOM	3370	D	TRP	A	612	15.184	13.348	12.978	1.00	9.78	8
ATOM	3318	CD1	HIS	A	406	35.504	5.164	5.733	1.00	18.12	7	ATOM	3371	H	ARG	A	413	15.184	13.348	12.978	1.00	10.07	7
ATOM	3319	CE1	HIS	A	406	35.318	4.505	4.578	1.00	16.95	6	ATOM	3372	CA	ARG	A	413	14.332	13.843	14.055	1.00	10.74	6
ATOM	3320	CE2	HIS	A	406	34.666	3.388	4.880	1.00	17.55	7	ATOM	3373	CB	ARG	A	413	14.635	15.236	14.615	1.00	8.23	6
ATOM	3321	C	HIS	A	406	33.580	7.002	8.026	1.00	13.47	6	ATOM	3374	CG	ARG	A	413	14.039	15.382	15.182	1.00	6.55	6
ATOM	3322	O	HIS	A	406	34.298	7.753	8.872	1.00	13.10	8	ATOM	3375	CD	ARG	A	413	16.262	14.604	16.464	1.00	6.58	6
ATOM	3323	H	ASP	A	407	32.841	7.500	7.048	1.00	13.42	7	ATOM	3376	HE	ARG	A	413	15.388	14.982	17.577	1.00	5.58	7
ATOM	3324	CA	ASP	A	407	32.837	8.877	6.628	1.00	13.27	6	ATOM	3377	CZ	ARG	A	413	15.602	16.062	18.326	1.00	8.01	6
ATOM	3325	CB	ASP	A	407	33.165	9.063	5.138	1.00	14.59	6	ATOM	3378	HE1	ARG	A	413	14.882	16.370	19.349	1.00	7.49	7
ATOM	3326	CG	ASP	A	407	34.556	8.665	4.654	1.00	14.13	6	ATOM	3379	HE2	ARG	A	413	16.645	16.870	18.094	1.00	7.46	7
ATOM	3327	CD1	ASP	A	407	35.474	8.360	5.486	1.00	14.23	8	ATOM	3380	C	ARG	A	413	12.946	13.767	13.403	1.00	11.41	6
ATOM	3328	CD2	ASP	A	407	34.808	8.646	5.381	1.00	18.58	6	ATOM	3381	O	ARG	A	413	12.678	14.374	12.355	1.00	11.24	8
ATOM	3329	C	ASP	A	407	31.457	9.532	6.757	1.00	12.98	6	ATOM	3382	H	GLU	A	414	12.076	12.980	14.035	1.00	12.08	7
ATOM	3330	D	ASP	A	407	31.310	10.601	7.368	1.00	12.77	8	ATOM	3383	CA	GLU	A	414	10.713	12.785	13.510	1.00	12.86	6
ATOM	3331	H	HIS	A	408	30.465	8.167	6.103	1.00	12.05	7	ATOM	3384	CB	GLU	A	414	10.578	11.626	14.195	1.00	11.98	6
ATOM	3332	CA	HIS	A	408	29.098	9.438	6.133	1.00	12.79	6	ATOM	3385	CG	GLU	A	414	10.578	10.270	13.880	1.00	12.67	6
ATOM	3333	CB	HIS	A	408	28.429	9.103	4.799	1.00	14.07	6	ATOM	3386	CD	GLU	A	414	9.722	9.123	14.401	1.00	14.64	6
ATOM	3334	CG2	HIS	A	408	27.045	4.656	9.742	1.00	13.86	6	ATOM	3387	CE1	GLU	A	414	8.485	9.240	14.504	1.00	14.73	8
ATOM	3335	CG1	HIS	A	408	29.251	9.578	3.597	1.00	13.69	6	ATOM	3388	CE2	GLU	A	414	10.249	8.841	14.723	1.00	15.78	8
ATOM	3336	CD1	HIS	A	408	28.979	8.781	2.321	1.00	14.63	6	ATOM	3389	CZ	GLU	A	414	9.819	14.015	13.605	1.00	13.32	6
ATOM	3337	C	HIS	A	408	28.219	7.260	7.260	1.00	12.80	6	ATOM	3390	O	GLU	A	414	8.855	14.606	12.864	1.00	13.17	8
ATOM	3338	D	HIS	A	408	27.838	7.712	7.271	1.00	12.81	8	ATOM	3391	H	GLY	A	415	10.096	15.006	14.389	1.00	14.06	7
ATOM	3339	H	VAL	A	409	27.191	9.762	8.193	1.00	12.85	7	ATOM	3392	CA	GLY	A	415	9.223	16.150	14.467	1.00	15.71	6

3393	C	GLY A 415	8.276	15.870	15.637	1.00	17.18	6	14.738	16.900	9.939	1.00	16.33	6
3394	O	GLY A 416	8.176	14.768	16.148	1.00	17.23	8	15.547	18.024	10.607	1.00	7.87	6
3395	N	ASP A 416	7.581	16.904	16.048	1.00	18.70	7	16.337	17.716	11.885	1.00	8.31	6
3396	CA	ASP A 416	6.606	16.860	17.118	1.00	20.18	6	17.570	16.854	11.716	1.00	6.45	6
3397	CA	ASP A 416	7.228	17.531	16.307	1.00	26.49	6	16.862	19.187	12.547	1.00	8.33	6
3398	CG	ASP A 416	6.358	17.615	19.535	1.00	31.33	6	15.577	15.630	9.781	1.00	10.11	6
3399	CG	ASP A 416	6.791	18.482	20.413	1.00	35.28	6	15.468	14.626	10.407	1.00	10.06	8
3400	CG	ASP A 416	5.301	16.975	19.696	1.00	32.88	8	16.469	15.658	8.706	1.00	9.69	7
3401	C	ASP A 416	5.400	17.597	16.568	1.00	21.08	6	17.366	14.543	6.361	1.00	9.38	6
3402	C	ASP A 416	5.423	18.631	15.908	1.00	20.94	8	16.885	13.742	7.143	1.00	6.73	6
3403	N	SER A 417	6.234	17.031	16.824	1.00	23.16	7	16.723	15.226	8.124	1.00	9.43	6
3404	CA	SER A 417	2.928	17.486	18.380	1.00	23.18	6	16.868	16.069	7.168	1.00	9.26	8
3405	CB	SER A 417	1.668	16.471	18.846	1.00	27.52	6	19.795	14.875	8.971	1.00	9.31	7
3406	CG	SER A 417	1.734	16.874	18.237	1.00	32.78	8	21.016	15.474	8.873	1.00	9.28	6
3407	C	SER A 417	2.585	18.852	16.929	1.00	23.50	6	21.436	16.106	10.234	1.00	9.50	6
3408	D	SER A 417	1.821	19.541	16.258	1.00	23.90	8	23.032	14.635	8.414	1.00	9.49	6
3409	N	SER A 418	3.145	19.217	18.073	1.00	23.61	7	21.989	13.294	8.823	1.00	9.20	8
3410	CA	SER A 418	2.982	20.541	18.628	1.00	23.56	6	22.965	14.846	7.581	1.00	9.04	7
3411	CB	SER A 418	3.247	20.523	20.135	1.00	24.90	6	24.057	14.016	7.090	1.00	10.53	6
3412	CG	SER A 418	4.660	20.195	20.198	1.00	27.24	8	23.734	13.630	5.656	1.00	11.90	6
3413	C	SER A 418	3.988	22.714	18.503	1.00	23.96	8	23.768	12.238	5.062	1.00	13.08	6
3414	C	SER A 418	3.995	22.714	18.503	1.00	23.96	8	23.768	12.238	5.062	1.00	13.08	6
3415	N	VAL A 419	4.894	21.195	17.094	1.00	23.44	7	25.327	14.877	7.098	1.00	10.73	6
3416	CA	VAL A 419	5.793	22.233	16.490	1.00	21.33	6	25.367	16.056	6.788	1.00	10.84	8
3417	CB	VAL A 419	7.278	22.269	16.815	1.00	19.53	6	26.460	14.406	7.520	1.00	10.83	7
3418	CG	VAL A 419	8.070	23.317	16.038	1.00	15.95	6	27.758	15.045	7.515	1.00	11.08	6
3419	C	VAL A 419	7.558	22.527	18.315	1.00	18.97	6	28.190	15.609	8.889	1.00	11.39	6
3420	C	VAL A 419	5.477	21.951	14.988	1.00	20.67	6	27.289	16.778	9.305	1.00	10.87	6
3421	D	VAL A 419	5.911	20.939	14.404	1.00	20.41	7	28.230	14.513	9.993	1.00	9.31	6
3422	N	ALA A 420	4.616	22.803	14.400	1.00	20.01	6	28.912	15.018	11.283	1.00	8.18	6
3423	CA	ALA A 420	4.174	22.558	13.017	1.00	19.28	6	28.779	14.006	6.996	1.00	11.33	6
3424	CB	ALA A 420	3.789	23.819	12.527	1.00	18.43	8	28.541	12.780	7.210	1.00	11.63	8
3425	C	ALA A 420	5.329	22.464	12.050	1.00	18.43	8	29.881	14.325	6.326	1.00	11.15	7
3426	D	ALA A 420	6.221	23.297	12.164	1.00	18.43	8	30.873	13.603	5.891	1.00	10.98	6
3427	N	ASN A 421	5.312	23.471	13.161	1.00	17.67	7	31.176	13.138	4.393	1.00	13.90	6
3428	CA	ASN A 421	6.356	21.242	10.168	1.00	16.69	6	30.085	13.558	3.592	1.00	14.12	8
3429	CB	ASN A 421	6.537	22.438	9.204	1.00	19.20	6	31.612	11.738	4.125	1.00	8.62	6
3430	CG	ASN A 421	5.312	22.617	8.330	1.00	21.29	6	32.346	14.119	6.111	1.00	10.97	6
3431	CG	ASN A 421	4.586	21.711	7.966	1.00	22.05	8	32.413	15.275	5.717	1.00	10.27	8
3432	CG	ASN A 421	5.028	23.853	7.994	1.00	23.75	7	33.213	13.328	6.685	1.00	11.50	7
3433	C	ASN A 421	7.760	28.891	10.703	1.00	15.64	6	34.540	13.958	6.672	1.00	11.94	6
3434	C	ASN A 421	8.711	29.946	9.931	1.00	15.23	8	35.391	13.652	7.861	1.00	11.35	6
3435	N	SER A 422	7.882	28.479	11.947	1.00	14.78	7	35.784	12.175	7.893	1.00	12.16	6
3436	CA	SER A 422	9.140	28.088	12.542	1.00	14.31	6	34.941	11.410	7.316	1.00	12.11	8
3437	CB	SER A 422	9.064	20.137	14.071	1.00	14.37	6	36.676	11.784	8.551	1.00	10.98	8
3438	CG	SER A 422	7.990	19.345	14.623	1.00	13.87	8	35.289	13.562	5.390	1.00	12.62	6
3439	C	SER A 422	9.518	18.705	12.009	1.00	13.67	6	36.452	13.961	5.293	1.00	12.99	8
3440	O	SER A 422	8.713	17.932	11.459	1.00	13.79	8	34.710	12.876	4.425	1.00	12.92	7
3441	N	GLY A 423	10.797	18.389	12.161	1.00	12.94	7	35.169	12.496	3.173	1.00	13.60	6
3442	CA	GLY A 423	11.329	17.066	11.679	1.00	12.05	6	34.647	12.693	1.981	1.00	13.83	6
3443	C	GLY A 423	12.546	17.472	10.825	1.00	11.56	6	33.681	13.671	1.929	1.00	13.86	8
3444	O	GLY A 423	12.532	18.566	10.232	1.00	11.46	8	34.509	11.820	0.999	1.00	14.36	7
3445	N	LEU A 424	13.562	16.612	10.738	1.00	10.94	7						

ATOM	3605	O	GLY A 446	4.984	14.124	-0.086	1.00	15.33	0	ATOM	3650	CG1	ILE A 452	17.009	29.640	6.443	1.00	14.27	6
ATOM	3606	N	GLU A 447	5.903	13.897	1.837	1.00	14.73	7	ATOM	3651	CD1	ILE A 452	16.275	25.551	7.802	1.00	14.37	6
ATOM	3607	CA	GLU A 447	6.387	15.280	1.807	1.00	14.28	6	ATOM	3652	C	ILE A 452	19.424	24.911	4.512	1.00	13.90	6
ATOM	3608	CB	GLU A 447	6.706	15.729	3.264	1.00	14.39	6	ATOM	3653	O	ILE A 452	19.482	26.146	4.529	1.00	13.78	8
ATOM	3609	CG	GLU A 447	5.369	15.838	4.018	1.00	13.77	6	ATOM	3654	HA	THR A 453	20.598	24.254	4.476	1.00	14.31	7
ATOM	3610	CD	GLU A 447	5.715	15.992	5.455	1.00	15.49	6	ATOM	3655	CA	THR A 453	21.885	24.911	4.427	1.00	14.90	6
ATOM	3611	CE1	GLU A 447	6.875	16.135	5.959	1.00	15.55	8	ATOM	3656	CB	THR A 453	23.065	23.977	4.697	1.00	12.74	6
ATOM	3612	CE2	GLU A 447	6.721	16.000	4.203	1.00	15.31	8	ATOM	3657	C	THR A 453	23.194	23.019	3.614	1.00	12.38	8
ATOM	3613	C	GLU A 447	7.644	15.680	1.041	1.00	13.72	6	ATOM	3658	CG2	THR A 453	22.184	25.480	3.030	1.00	15.80	6
ATOM	3614	O	GLU A 447	8.494	14.838	0.929	1.00	13.70	8	ATOM	3659	O	THR A 453	23.073	26.280	2.774	1.00	15.75	8
ATOM	3615	N	THR A 448	7.703	16.924	0.404	1.00	13.28	7	ATOM	3660	H	GLY A 454	21.475	24.968	2.016	1.00	16.49	7
ATOM	3616	CA	THR A 448	8.904	17.368	-0.059	1.00	13.29	6	ATOM	3661	CA	GLY A 454	21.614	25.345	0.622	1.00	16.88	6
ATOM	3618	CG1	THR A 448	8.881	18.432	-1.179	1.00	14.50	6	ATOM	3662	C	GLY A 454	22.752	24.598	-0.055	1.00	17.42	6
ATOM	3619	CG2	THR A 448	7.898	17.829	-2.231	1.00	16.23	8	ATOM	3663	H	ASX A 455	22.987	24.858	-1.237	1.00	17.55	8
ATOM	3620	C	THR A 448	9.966	18.972	-1.787	1.00	12.12	8	ATOM	3664	CA	ASX A 455	23.496	23.700	0.548	1.00	17.75	7
ATOM	3621	O	THR A 448	9.440	19.038	0.994	1.00	12.85	6	ATOM	3665	CB	ASX A 455	26.145	23.158	1.831	1.00	19.02	6
ATOM	3622	H	TRP A 449	11.021	17.508	1.627	1.00	12.81	8	ATOM	3666	CG1	ASN A 456	24.847	21.968	-1.217	1.00	18.75	6
ATOM	3623	CA	TRP A 449	12.011	18.049	2.095	1.00	12.53	7	ATOM	3667	C	ASN A 456	22.863	22.827	3.103	1.00	17.34	7
ATOM	3624	CB	TRP A 449	12.564	16.992	3.035	1.00	9.67	6	ATOM	3668	CG2	ASN A 456	24.847	21.968	-1.217	1.00	18.75	6
ATOM	3625	CG	TRP A 449	13.161	15.756	4.129	1.00	9.46	6	ATOM	3669	O	ASN A 456	22.863	21.968	-1.217	1.00	18.75	6
ATOM	3626	CG2	TRP A 449	10.762	15.974	4.129	1.00	9.46	6	ATOM	3670	CA	ASN A 456	22.863	21.968	-1.217	1.00	18.75	6
ATOM	3627	CG1	TRP A 449	9.710	16.416	5.351	1.00	9.60	6	ATOM	3671	C	ASN A 456	22.863	21.968	-1.217	1.00	18.75	6
ATOM	3628	CG2	TRP A 449	10.750	15.445	7.438	1.00	9.93	6	ATOM	3672	O	ASN A 456	22.863	21.968	-1.217	1.00	18.75	6
ATOM	3629	CG3	TRP A 449	13.193	15.216	7.286	1.00	7.79	6	ATOM	3673	H	ASN A 456	23.079	17.230	-1.408	1.00	23.06	6
ATOM	3630	CG4	TRP A 449	11.953	15.068	7.958	1.00	8.43	6	ATOM	3674	CA	ASN A 456	22.752	16.607	-2.676	1.00	23.06	6
ATOM	3631	C	TRP A 449	13.168	18.731	1.320	1.00	12.82	6	ATOM	3675	CB	ARG A 456	23.472	16.017	-3.613	1.00	29.89	6
ATOM	3632	O	TRP A 449	13.563	18.178	0.275	1.00	12.82	6	ATOM	3676	CG	ARG A 456	22.869	15.821	-4.631	1.00	29.42	7
ATOM	3633	CA	HIS A 450	13.727	19.836	1.779	1.00	13.04	7	ATOM	3677	C	ARG A 456	20.994	21.388	-2.721	1.00	36.25	7
ATOM	3634	CB	HIS A 450	14.852	20.452	1.846	1.00	13.34	6	ATOM	3678	CG1	ARG A 456	20.777	21.809	-1.881	1.00	39.69	6
ATOM	3635	CG	HIS A 450	14.596	21.682	0.331	1.00	14.62	6	ATOM	3679	O	ARG A 456	20.777	21.809	-1.881	1.00	39.69	6
ATOM	3636	CG2	HIS A 450	14.289	22.083	1.191	1.00	17.87	6	ATOM	3680	H	SER A 457	19.533	22.134	-4.032	1.00	39.78	7
ATOM	3637	C	TRP A 449	16.886	24.101	1.061	1.00	19.94	6	ATOM	3681	CA	SER A 457	19.748	23.040	-5.741	1.00	29.18	6
ATOM	3638	H	HIS A 450	13.563	18.178	0.275	1.00	12.82	6	ATOM	3682	CB	SER A 457	20.301	22.068	-6.668	1.00	28.86	8
ATOM	3639	CA	HIS A 450	13.727	19.836	1.779	1.00	13.04	7	ATOM	3683	C	SER A 457	18.439	21.136	-4.883	1.00	19.94	6
ATOM	3640	CB	HIS A 450	14.852	20.452	1.846	1.00	13.34	6	ATOM	3684	CG	SER A 457	17.317	21.592	-5.183	1.00	20.37	8
ATOM	3641	CG	HIS A 450	14.596	21.682	0.331	1.00	14.62	6	ATOM	3685	H	GLU A 458	18.708	19.841	-4.835	1.00	19.72	7
ATOM	3642	CG2	HIS A 450	14.289	22.083	1.191	1.00	17.87	6	ATOM	3686	CA	GLU A 458	17.687	18.883	-5.161	1.00	19.82	6
ATOM	3643	C	TRP A 449	16.886	24.101	1.061	1.00	19.94	6	ATOM	3687	CB	GLU A 458	18.321	17.611	-5.803	1.00	24.71	6
ATOM	3644	H	HIS A 450	13.563	18.178	0.275	1.00	12.82	6	ATOM	3688	CG	GLU A 458	17.134	17.001	-6.543	1.00	31.90	6
ATOM	3645	CA	HIS A 450	13.727	19.836	1.779	1.00	13.04	7	ATOM	3689	CG1	GLU A 458	17.352	15.435	-7.168	1.00	36.18	6
ATOM	3646	CB	HIS A 450	14.852	20.452	1.846	1.00	13.34	6	ATOM	3690	CG2	GLU A 458	18.250	15.229	-7.681	1.00	38.60	8
ATOM	3647	CG	HIS A 450	14.596	21.682	0.331	1.00	14.62	6	ATOM	3691	C	GLU A 458	16.057	16.979	-7.142	1.00	38.01	8
ATOM	3648	C	TRP A 449	16.886	24.101	1.061	1.00	19.94	6	ATOM	3692	O	GLU A 458	16.057	16.979	-7.142	1.00	38.01	8
ATOM	3649	H	HIS A 450	13.563	18.178	0.275	1.00	12.82	6	ATOM	3693	CA	SER A 457	18.850	18.407	-3.978	1.00	19.28	4
ATOM	3650	CA	HIS A 450	13.727	19.836	1.779	1.00	13.04	7	ATOM	3694	CB	SER A 457	17.375	17.778	-3.068	1.00	19.23	8
ATOM	3651	CB	HIS A 450	14.852	20.452	1.846	1.00	13.34	6	ATOM	3695	CG	SER A 457	15.545	18.628	-4.028	1.00	18.75	7
ATOM	3652	CG	HIS A 450	14.596	21.682	0.331	1.00	14.62	6	ATOM	3696	H	GLU A 458	14.893	19.401	-5.083	1.00	18.49	6
ATOM	3653	C	TRP A 449	16.886	24.101	1.061	1.00	19.94	6	ATOM	3697	CA	SER A 457	14.611	18.231	-2.974	1.00	18.56	6
ATOM	3654	H	HIS A 450	13.563	18.178	0.275	1.00	12.82	6	ATOM	3698	CB	SER A 457	13.270	18.916	-3.298	1.00	18.40	6
ATOM	3655	CA	HIS A 450	13.727	19.836	1.779	1.00	13.04	7	ATOM	3699	CG	SER A 457						
ATOM	3656	CB	HIS A 450	14.852	20.452	1.846	1.00	13.34	6	ATOM	3700	C	GLU A 458						
ATOM	3657	CG	HIS A 450	14.596	21.682	0.331	1.00	14.62	6	ATOM	3701	CA	SER A 457						
ATOM	3658	C	TRP A 449	16.886	24.101	1.061	1.00	19.94	6	ATOM	3702	CB	SER A 457						
ATOM	3659	H	HIS A 450	13.563	18.178	0.275	1.00	12.82	6	ATOM	3703	C	GLU A 458						
ATOM	3660	CA	HIS A 450	13.727	19.836	1.779	1.00	13.04	7	ATOM	3704	CG	GLU A 458						
ATOM	3661	CB	HIS A 450	14.852	20.452	1.846	1.00	13.34	6	ATOM	3705	CG1	GLU A 458						
ATOM	3662	CG	HIS A 450	14.596	21.682	0.331	1.00	14.62	6	ATOM	3706	CG2	GLU A 458						
ATOM	3663	C	TRP A 449	16.886	24.101	1.061	1.00	19.94	6	ATOM	3707	C	GLU A 458						
ATOM	3664	H	HIS A 450	13.563	18.178	0.275	1.00	12.82	6	ATOM	3708	CA	GLU A 458						
ATOM	3665	CA	HIS A 450	13.727	19.836	1.779	1.00	13.04	7	ATOM	3709	CB	GLU A 458						
ATOM	3666	CB	HIS A 450	14.852	20.452	1.846	1.00	13.34	6	ATOM	3710	C	GLU A 458						
ATOM	3667	CG	HIS A 450	14.596	21.682	0.331	1.00	14.62	6	ATOM	3711	O	GLU A 458						

AT04	3711	CG	PRO A 459	13.637	19.885	-4.393	1.00 18.37	6	AT04	3764	CA	18P A 467	11.850	6.686	4.486	1.00 20.35	6
AT04	3712	C	PRO A 459	14.504	16.723	-2.859	1.00 18.67	6	AT04	3765	CB	18P A 467	12.439	5.313	4.107	1.00 20.44	6
AT04	3713	D	PRO A 459	14.889	15.979	-3.780	1.00 18.66	6	AT04	3766	CG	18P A 467	12.372	4.283	5.181	1.00 20.04	6
AT04	3714	H	VAL A 460	14.113	16.146	-1.728	1.00 18.24	7	AT04	3767	CD	18P A 467	13.427	3.771	5.993	1.00 19.41	6
AT04	3715	CA	VAL A 460	13.987	14.691	-1.304	1.00 18.19	6	AT04	3768	CE	18P A 467	12.844	2.826	6.880	1.00 19.61	6
AT04	3716	CB	VAL A 460	14.908	14.168	-0.379	1.00 17.56	6	AT04	3769	CE3	18P A 467	14.883	3.987	6.049	1.00 18.58	6
AT04	3717	CE1	VAL A 460	14.719	12.685	-0.976	1.00 17.48	6	AT04	3770	CE1	18P A 467	11.227	3.633	5.591	1.00 20.26	6
AT04	3718	CE2	VAL A 460	16.371	14.396	-0.750	1.00 17.31	6	AT04	3771	HE1	18P A 467	11.487	2.779	6.422	1.00 19.67	7
AT04	3719	C	VAL A 460	15.528	14.396	-1.309	1.00 18.23	6	AT04	3772	CE2	18P A 467	13.593	2.302	7.824	1.00 19.59	6
AT04	3720	O	VAL A 460	11.892	15.157	-0.428	1.00 18.51	8	AT04	3773	CE3	18P A 467	15.552	3.268	6.997	1.00 20.04	6
AT04	3721	H	VAL A 461	11.894	13.362	-1.798	1.00 18.03	7	AT04	3774	CE2	18P A 467	14.999	2.315	7.868	1.00 19.86	6
AT04	3722	CA	VAL A 461	10.468	13.103	-1.458	1.00 17.66	6	AT04	3775	C	18P A 467	12.174	7.831	3.312	1.00 20.06	6
AT04	3723	CB	VAL A 461	9.584	12.863	-2.709	1.00 17.06	6	AT04	3776	O	18P A 467	11.355	7.837	2.613	1.00 19.99	6
AT04	3724	CE1	VAL A 461	8.143	12.584	-2.856	1.00 16.42	6	AT04	3777	H	GLY A 468	13.356	8.193	3.372	1.00 19.55	7
AT04	3725	CE2	VAL A 461	9.629	14.023	-3.878	1.00 15.12	6	AT04	3778	CA	GLY A 468	13.838	9.103	2.345	1.00 19.08	6
AT04	3726	C	VAL A 461	10.418	11.943	-0.456	1.00 17.45	6	AT04	3779	C	GLY A 468	15.293	8.667	2.044	1.00 18.67	6
AT04	3727	O	VAL A 461	11.046	10.893	-0.596	1.00 17.01	8	AT04	3780	O	GLY A 468	15.969	8.121	2.908	1.00 18.51	8
AT04	3728	H	ILE A 462	9.707	12.111	0.447	1.00 17.69	7	AT04	3781	H	GLU A 469	15.761	8.896	0.848	1.00 18.42	7
AT04	3729	CA	ILE A 462	9.596	11.050	1.642	1.00 18.12	6	AT04	3782	CA	GLU A 469	17.153	8.577	0.487	1.00 18.35	6
AT04	3730	CB	ILE A 462	9.212	11.549	3.046	1.00 15.81	6	AT04	3783	CB	GLU A 469	17.287	7.714	-0.771	1.00 23.55	6
AT04	3731	CE3	ILE A 462	9.222	10.334	3.984	1.00 15.11	6	AT04	3784	CE	GLU A 469	18.710	7.626	-1.293	1.00 29.59	6
AT04	3732	CE1	ILE A 462	10.089	12.691	3.597	1.00 13.00	6	AT04	3785	CE	GLU A 469	18.967	7.178	-2.729	1.00 34.28	6
AT04	3733	CE1	ILE A 462	11.575	12.439	3.642	1.00 9.27	6	AT04	3786	CE1	GLU A 469	19.831	6.252	-2.904	1.00 36.09	8
AT04	3734	C	ILE A 462	8.554	10.036	1.116	1.00 18.85	6	AT04	3787	CE2	GLU A 469	18.340	7.755	-3.681	1.00 35.52	8
AT04	3735	O	ILE A 462	7.432	10.390	0.717	1.00 18.87	7	AT04	3788	C	GLU A 469	17.805	9.964	0.424	1.00 17.57	8
AT04	3736	H	ASN A 463	8.922	8.755	1.538	1.00 19.55	8	AT04	3789	O	GLU A 469	17.555	10.801	-0.433	1.00 17.46	8
AT04	3737	CA	ASN A 463	8.090	7.650	0.672	1.00 20.49	6	AT04	3790	H	PHE A 470	18.666	10.297	1.388	1.00 17.09	7
AT04	3738	CB	ASN A 463	8.940	6.443	0.342	1.00 20.20	6	AT04	3791	CA	PHE A 470	19.246	11.860	1.415	1.00 16.47	6
AT04	3739	CG	ASN A 463	9.411	5.430	1.361	1.00 21.59	6	AT04	3792	CB	PHE A 470	19.076	12.181	2.850	1.00 14.77	6
AT04	3740	CE1	ASN A 463	9.117	5.376	2.579	1.00 22.11	8	AT04	3793	CG	PHE A 470	17.686	12.126	3.451	1.00 11.90	6
AT04	3741	CE2	ASN A 463	10.221	4.455	0.984	1.00 19.99	7	AT04	3794	CE1	PHE A 470	17.501	11.841	4.208	1.00 11.94	6
AT04	3742	C	ASN A 463	6.975	7.297	1.630	1.00 21.45	6	AT04	3795	CE2	PHE A 470	16.823	13.197	3.296	1.00 10.16	6
AT04	3743	O	ASN A 463	6.884	7.742	2.770	1.00 31.42	8	AT04	3796	CE1	PHE A 470	16.037	11.030	4.790	1.00 11.36	6
AT04	3744	H	SER A 464	6.070	6.590	1.173	1.00 22.31	7	AT04	3797	CE2	PHE A 470	15.562	13.155	3.871	1.00 9.61	6
AT04	3745	CA	SER A 464	6.877	5.971	1.916	1.00 22.97	6	AT04	3798	C2	PHE A 470	15.159	12.069	4.605	1.00 9.27	6
AT04	3746	CB	SER A 464	3.915	5.159	1.024	1.00 23.92	6	AT04	3799	C	PHE A 470	20.682	11.731	0.945	1.00 16.14	6
AT04	3747	CG	SER A 464	4.565	3.841	0.731	1.00 25.49	8	AT04	3800	O	PHE A 470	21.406	10.761	1.154	1.00 16.37	8
AT04	3748	C	SER A 464	5.187	5.303	3.248	1.00 23.29	6	AT04	3801	H	HIS A 471	21.142	12.867	0.363	1.00 15.78	7
AT04	3749	O	SER A 464	4.319	5.600	6.131	1.00 23.52	8	AT04	3802	CA	HIS A 471	22.462	13.007	-0.146	1.00 15.69	6
AT04	3750	H	GLU A 465	6.344	4.722	3.468	1.00 23.48	7	AT04	3803	CB	HIS A 471	22.332	13.373	-1.455	1.00 17.00	6
AT04	3751	CA	GLU A 465	6.816	4.134	4.708	1.00 23.73	6	AT04	3804	CG	HIS A 471	21.894	12.216	-2.515	1.00 20.58	6
AT04	3752	CB	GLU A 465	7.931	3.164	4.313	1.00 29.98	6	AT04	3805	CG	HIS A 471	22.588	11.406	-3.372	1.00 21.49	6
AT04	3753	CG	GLU A 465	7.852	1.671	4.516	1.00 35.99	6	AT04	3806	CE1	HIS A 471	20.560	11.780	-2.567	1.00 22.05	7
AT04	3754	C	GLU A 465	6.542	1.117	3.976	1.00 39.49	6	AT04	3807	CE1	HIS A 471	20.481	10.745	-3.399	1.00 21.74	6
AT04	3755	CE1	GLU A 465	6.607	1.177	2.734	1.00 41.53	8	AT04	3808	CE2	HIS A 471	21.688	10.491	-3.900	1.00 22.49	7
AT04	3756	CE2	GLU A 465	5.709	0.684	4.812	1.00 41.27	8	AT04	3809	O	HIS A 471	23.282	14.111	0.594	1.00 15.47	6
AT04	3757	C	GLU A 465	7.511	5.095	5.721	1.00 23.78	8	AT04	3810	O	HIS A 471	22.727	15.102	0.997	1.00 15.28	8
AT04	3758	O	GLU A 465	7.857	4.472	6.848	1.00 23.24	8	AT04	3811	H	VAL A 472	24.618	13.993	0.446	1.00 15.23	7
AT04	3759	H	GLY A 466	7.746	6.345	5.354	1.00 22.53	7	AT04	3812	CA	VAL A 472	25.529	14.978	0.964	1.00 15.01	6
AT04	3760	CA	GLY A 466	6.436	7.317	6.135	1.00 21.95	6	AT04	3813	CB	VAL A 472	26.385	14.698	2.271	1.00 16.48	6
AT04	3761	C	GLY A 466	9.969	7.245	5.909	1.00 21.47	6	AT04	3814	CE1	VAL A 472	26.281	15.727	3.368	1.00 15.07	6
AT04	3762	O	GLY A 466	10.728	7.644	6.828	1.00 21.33	8	AT04	3815	CE2	VAL A 472	26.275	13.374	2.750	1.00 17.25	6
AT04	3763	H	18P A 467	10.441	6.770	4.751	1.00 20.79	7	AT04	3816	C	VAL A 472	26.730	15.285	0.001	1.00 14.42	6

ATOM	3817	D	VAL A 472	27.246	16.169	-0.462	1.00	14.29	8
ATOM	3818	R	ASR A 473	27.200	16.444	-0.101	1.00	13.78	7
ATOM	3819	CA	ASR A 473	28.404	16.662	-0.801	1.00	13.30	6
ATOM	3820	CB	ASR A 473	28.514	18.108	-1.339	1.00	13.44	6
ATOM	3821	CG	ASR A 473	27.403	18.519	-2.301	1.00	15.11	6
ATOM	3822	CG1	ASR A 473	26.781	17.837	-2.882	1.00	15.07	8
ATOM	3823	CG2	ASR A 473	27.148	19.803	-2.494	1.00	15.52	7
ATOM	3824	C	ASR A 473	29.633	16.278	-0.066	1.00	12.99	6
ATOM	3825	O	ASR A 473	29.567	16.164	1.139	1.00	12.88	8
ATOM	3826	R	GLY A 474	30.792	16.046	-0.723	1.00	12.57	7
ATOM	3827	CA	GLY A 474	32.004	15.690	0.826	1.00	11.90	6
ATOM	3828	C	GLY A 474	32.429	16.874	0.897	1.00	11.47	6
ATOM	3829	O	GLY A 474	32.305	18.054	0.534	1.00	11.68	8
ATOM	3830	R	GLY A 475	32.940	16.534	2.058	1.00	10.93	7
ATOM	3831	CA	GLY A 475	33.425	17.392	3.139	1.00	10.37	6
ATOM	3832	C	GLY A 475	32.350	18.425	3.486	1.00	10.04	6
ATOM	3833	O	GLY A 475	32.646	19.606	3.607	1.00	9.82	8
ATOM	3834	R	SEB A 476	31.076	17.953	3.556	1.00	9.71	7
ATOM	3835	CA	SEB A 476	29.967	18.862	3.748	1.00	9.25	6
ATOM	3836	C	SEB A 476	28.910	18.374	4.718	1.00	8.87	6
ATOM	3837	OG	SEB A 476	28.487	20.170	2.237	1.00	11.03	8
ATOM	3838	O	SEB A 476	28.982	17.301	5.311	1.00	8.60	8
ATOM	3839	R	VAL A 477	27.865	19.207	4.864	1.00	8.73	7
ATOM	3840	CA	VAL A 477	26.711	18.975	5.699	1.00	8.42	6
ATOM	3841	CB	VAL A 477	26.705	19.802	7.028	1.00	8.94	6
ATOM	3842	CB	VAL A 477	25.389	19.640	7.754	1.00	5.67	6
ATOM	3843	CG1	VAL A 477	26.953	21.281	6.811	1.00	5.00	6
ATOM	3844	CG2	VAL A 477	25.462	19.333	4.887	1.00	8.35	6
ATOM	3845	C	VAL A 477	24.603	18.567	5.033	1.00	8.45	7
ATOM	3846	O	VAL A 477	23.087	18.781	4.462	1.00	8.34	6
ATOM	3847	R	SEB A 478	22.792	17.840	3.254	1.00	8.85	6
ATOM	3848	CA	SEB A 478	23.251	18.520	2.073	1.00	11.98	8
ATOM	3849	CB	SEB A 478	22.074	18.693	5.374	1.00	8.16	6
ATOM	3850	OG	SEB A 478	22.181	17.527	6.326	1.00	7.79	8
ATOM	3851	C	SEB A 478	21.114	19.406	5.720	1.00	8.43	7
ATOM	3852	O	SEB A 478	20.039	19.323	6.693	1.00	8.49	6
ATOM	3853	R	ILE A 479	20.160	20.274	7.864	1.00	8.78	6
ATOM	3854	CA	ILE A 479	18.976	19.999	8.846	1.00	6.48	6
ATOM	3855	CB	ILE A 479	21.502	20.102	8.847	1.00	8.82	6
ATOM	3856	CG1	ILE A 479	21.914	21.342	9.399	1.00	7.53	6
ATOM	3857	CG2	ILE A 479	18.689	19.539	6.013	1.00	8.75	6
ATOM	3858	C	ILE A 479	18.346	20.671	5.734	1.00	8.74	7
ATOM	3859	O	ILE A 479	17.969	18.447	5.701	1.00	9.32	7
ATOM	3860	R	THR A 480	16.682	18.457	5.141	1.00	10.04	6
ATOM	3861	CA	THR A 480	16.431	17.093	4.465	1.00	10.47	6
ATOM	3862	CB	THR A 480	17.358	16.901	3.299	1.00	11.51	6
ATOM	3863	CG	THR A 480	19.620	16.314	3.605	1.00	12.15	6
ATOM	3864	CG1	THR A 480	19.531	16.102	2.589	1.00	12.53	6
ATOM	3865	CG2	THR A 480	17.080	17.306	2.001	1.00	11.63	6
ATOM	3866	C	THR A 480	17.112	17.112	0.998	1.00	12.21	6
ATOM	3867	O	THR A 480	19.177	16.496	1.294	1.00	12.89	6
ATOM	3868	R	THR A 480	15.497	18.650	4.064	1.00	10.40	8
ATOM	3869	CA	THR A 480	15.416	18.002	7.124	1.00	10.50	8
ATOM	3870	CB	THR A 480	13.420	19.904	6.431	1.00	11.15	7
ATOM	3871	CG	THR A 480	13.545	21.252	7.239	1.00	12.11	6
ATOM	3872	CG1	THR A 480	14.600	21.080	8.319	1.00	10.53	6
ATOM	3873	CG2	THR A 480	13.880	22.458	6.409	1.00	7.87	6
ATOM	3874	C	THR A 480	12.268	20.186	5.458	1.00	13.24	8
ATOM	3875	O	THR A 480	12.481	20.334	4.256	1.00	13.31	8
ATOM	3876	R	GLN A 482	11.060	20.080	5.969	1.00	14.41	7
ATOM	3877	CA	GLN A 482	9.911	20.338	5.064	1.00	15.58	6
ATOM	3878	CB	GLN A 482	8.631	20.338	5.896	1.00	18.30	6
ATOM	3879	CG	GLN A 482	7.544	21.053	5.090	1.00	23.44	6
ATOM	3880	CG1	GLN A 482	6.745	20.125	4.176	1.00	25.41	6
ATOM	3881	CG2	GLN A 482	6.283	19.165	4.785	1.00	25.61	8
ATOM	3882	C	GLN A 482	6.540	20.395	2.875	1.00	25.49	7
ATOM	3883	O	GLN A 482	10.086	21.558	4.246	1.00	16.28	6
ATOM	3884	R	ARG A 483	10.404	22.646	4.755	1.00	16.41	8
ATOM	3885	CA	ARG A 483	9.856	21.490	2.934	1.00	17.07	6
ATOM	3886	CB	ARG A 483	9.955	22.625	2.026	1.00	17.07	6
ATOM	3887	CG	ARG A 483	9.913	22.081	0.609	1.00	18.13	6
ATOM	3888	CG1	ARG A 483	9.621	23.031	-0.524	1.00	19.83	6
ATOM	3889	CG2	ARG A 483	10.817	23.756	-1.071	1.00	22.10	6
ATOM	3890	C	ARG A 483	11.199	24.865	-0.224	1.00	24.98	7
ATOM	3891	O	ARG A 483	11.940	25.939	-0.498	1.00	26.41	6
ATOM	3892	R	ARG A 483	12.515	26.296	-1.651	1.00	26.83	7
ATOM	3893	CA	ARG A 483	12.081	28.726	-0.575	1.00	27.28	7
ATOM	3894	CB	ARG A 483	8.817	23.598	2.308	1.00	17.44	6
ATOM	3895	CG	ARG A 483	9.004	24.833	2.203	1.00	17.83	8
ATOM	3896	CG1	ARG A 483	7.689	23.159	2.631	1.00	18.43	8
ATOM	3897	CG2	ARG A 483	44.093	25.586	51.930	1.00	10.30	20
ATOM	3898	C	ARG A 483	43.109	26.983	43.727	1.00	8.87	20
ATOM	3899	O	ARG A 483	36.437	9.091	7.752	1.00	19.31	20
ATOM	3900	R	ILE A 501	5.896	16.803	8.528	1.00	17.57	20
ATOM	3901	CA	ILE A 501	46.182	29.694	41.805	1.00	5.00	8
ATOM	3902	CB	ILE A 501	39.434	45.537	34.032	1.00	7.97	8
ATOM	3903	CG	ILE A 501	35.632	30.198	39.664	1.00	5.16	8
ATOM	3904	CG1	ILE A 501	31.019	26.580	20.005	1.00	5.00	8
ATOM	3905	CG2	ILE A 501	34.344	20.929	31.664	1.00	7.18	8
ATOM	3906	C	ILE A 501	24.507	18.918	21.861	1.00	11.28	8
ATOM	3907	O	ILE A 501	38.313	44.279	32.223	1.00	6.82	8
ATOM	3908	R	THR A 480	39.626	39.129	42.515	1.00	5.00	8
ATOM	3909	CA	THR A 480	30.223	47.484	41.150	1.00	8.45	8
ATOM	3910	CB	THR A 480	35.182	46.470	25.198	1.00	13.57	8
ATOM	3911	CG	THR A 480	39.320	23.455	35.030	1.00	5.58	8
ATOM	3912	CG1	THR A 480	39.029	37.148	61.342	1.00	6.36	8
ATOM	3913	CG2	THR A 480	51.724	19.710	23.165	1.00	13.82	8
ATOM	3914	C	THR A 480	5.684	18.660	1.889	1.00	5.27	8
ATOM	3915	O	THR A 480	38.823	36.243	42.467	1.00	5.00	8
ATOM	3916	R	THR A 480	37.438	41.452	45.589	1.00	13.75	8
ATOM	3917	CA	THR A 480	14.634	9.750	20.928	1.00	7.22	8
ATOM	3918	CB	THR A 480	38.712	30.913	38.542	1.00	7.22	8

A104	4029	0405	0405	13	13.009	12.182	-4.047	1.00	27.61	0	4082	0408	0408	18	30.748	53.658	50.670	1.00	29.38	0
A104	4030	0406	0406	13	12.756	8.582	1.824	1.00	29.04	0	4083	0409	0409	18	50.045	24.808	35.502	1.00	35.76	0
A104	4031	0407	0407	13	16.349	23.415	-2.919	1.00	36.05	0	4084	0410	0410	19	23.202	19.032	28.774	1.00	27.27	0
A104	4032	0408	0408	13	36.916	48.802	51.068	1.00	13.92	0	4085	0411	0411	19	54.614	46.941	48.285	1.00	29.46	0
A104	4033	0409	0409	13	36.916	48.802	51.068	1.00	27.25	0	4086	0412	0412	19	46.049	21.147	25.386	1.00	31.35	0
A104	4034	0410	0410	13	44.576	23.979	15.915	1.00	39.18	0	4087	0413	0413	19	45.816	49.038	43.196	1.00	33.55	0
A104	4035	0411	0411	14	16.344	4.264	16.031	1.00	22.00	0	4088	0414	0414	19	22.659	43.614	47.566	1.00	46.32	0
A104	4036	0412	0412	14	32.347	13.546	-3.049	1.00	37.27	0	4089	0415	0415	19	60.822	30.153	59.870	1.00	43.42	0
A104	4037	0413	0413	14	45.366	38.058	33.758	1.00	20.90	0	4090	0416	0416	19	32.544	1.677	6.989	1.00	38.69	0
A104	4038	0414	0414	14	4.549	18.600	13.099	1.00	20.30	0	4091	0417	0417	19	58.647	31.408	43.808	1.00	33.78	0
A104	4039	0415	0415	14	15.354	36.796	43.569	1.00	18.79	0	4092	0418	0418	19	16.948	27.505	19.812	1.00	23.95	0
A104	4040	0416	0416	14	44.863	30.462	37.791	1.00	33.45	0	4093	0419	0419	19	6.318	5.129	-1.860	1.00	55.10	0
A104	4041	0417	0417	14	23.136	23.195	37.475	1.00	31.43	0	4094	0420	0420	19	32.149	29.484	1.396	1.00	29.24	0
A104	4042	0418	0418	14	30.694	15.659	-3.842	1.00	23.59	0	4095	0421	0421	20	18.952	20.628	24.894	1.00	35.86	0
A104	4043	0419	0419	14	39.010	7.257	14.525	1.00	37.98	0	4096	0422	0422	20	31.733	56.172	34.803	1.00	38.99	0
A104	4044	0420	0420	15	37.998	55.360	32.899	1.00	35.04	0	4097	0423	0423	20	54.293	14.452	58.415	1.00	35.67	0
A104	4045	0421	0421	15	21.133	44.448	35.681	1.00	35.84	0	4098	0424	0424	20	25.114	53.998	30.655	1.00	43.33	0
A104	4046	0422	0422	15	23.993	4.153	14.519	1.00	20.07	0	4099	0425	0425	20	43.966	46.509	55.136	1.00	37.54	0
A104	4047	0423	0423	15	21.568	23.231	44.662	1.00	34.60	0	4100	0426	0426	20	58.366	45.019	48.175	1.00	43.14	0
A104	4048	0424	0424	15	9.185	24.646	6.708	1.00	19.79	0	4101	0427	0427	20	44.205	21.201	13.125	1.00	51.53	0
A104	4049	0425	0425	15	44.580	35.812	31.349	1.00	48.30	0	4102	0428	0428	20	61.128	25.014	42.919	1.00	34.86	0
A104	4050	0426	0426	15	30.789	25.745	52.371	1.00	38.63	0	4103	0429	0429	20	48.371	24.444	12.113	1.00	45.95	0
A104	4051	0427	0427	15	41.284	38.972	11.603	1.00	29.22	0	4104	0430	0430	20	18.370	31.505	12.739	1.00	27.20	0
A104	4052	0428	0428	15	56.979	36.187	58.016	1.00	37.19	0	4105	0431	0431	20	33.430	25.045	51.739	1.00	31.92	0
A104	4053	0429	0429	15	25.886	5.827	3.524	1.00	21.64	0	4106	0432	0432	20	47.668	31.418	59.018	1.00	35.64	0
A104	4054	0430	0430	16	41.289	14.341	39.346	1.00	28.91	0	4107	0433	0433	20	43.308	25.115	12.609	1.00	40.37	0
A104	4055	0431	0431	16	20.238	10.905	31.899	1.00	18.69	0	4108	0434	0434	20	44.725	50.787	28.523	1.00	26.83	0
A104	4056	0432	0432	16	44.542	44.756	52.978	1.00	20.62	0	4109	0435	0435	20	40.073	41.591	56.477	1.00	38.23	0
A104	4057	0433	0433	16	57.377	17.228	51.604	1.00	22.46	0	4110	0436	0436	20	3.706	15.718	9.641	1.00	23.55	0
A104	4058	0434	0434	16	35.851	33.580	56.957	1.00	30.96	0	4111	0437	0437	20	46.527	18.870	50.827	1.00	35.55	0
A104	4059	0435	0435	16	35.776	25.007	52.963	1.00	35.92	0	4112	0438	0438	20	51.052	12.865	45.183	1.00	48.72	0
A104	4060	0436	0436	16	50.697	28.378	37.894	1.00	17.69	0	4113	0439	0439	20	54.191	42.505	55.913	1.00	22.39	0
A104	4061	0437	0437	16	41.297	31.972	30.943	1.00	23.15	0	4114	0440	0440	20	65.480	31.263	47.436	1.00	36.62	0
A104	4062	0438	0438	16	60.184	21.780	53.887	1.00	24.69	0	4115	0441	0441	20	30.283	47.935	54.169	1.00	31.71	0
A104	4063	0439	0439	16	33.939	36.911	56.317	1.00	28.54	0	4116	0442	0442	20	35.283	36.318	46.899	1.00	68.21	0
A104	4064	0440	0440	17	27.783	49.620	50.985	1.00	21.73	0	4117	0443	0443	20	47.871	46.056	38.969	1.00	32.78	0
A104	4065	0441	0441	17	38.322	12.309	23.483	1.00	42.93	0	4118	0444	0444	20	37.896	8.826	3.495	1.00	35.54	0
A104	4066	0442	0442	17	19.759	16.587	26.896	1.00	25.91	0	4119	0445	0445	20	35.101	8.638	38.130	1.00	35.44	0
A104	4067	0443	0443	17	18.392	24.561	-0.866	1.00	45.44	0	4120	0446	0446	20	38.368	4.945	9.283	1.00	39.44	0
A104	4068	0444	0444	17	43.370	16.553	29.268	1.00	24.28	0	4121	0447	0447	20	29.192	42.186	18.601	1.00	35.54	0
A104	4069	0445	0445	17	12.908	25.520	6.810	1.00	39.21	0	4122	0448	0448	20	43.449	25.207	33.605	1.00	42.65	0
A104	4070	0446	0446	17	48.009	35.484	9.586	1.00	24.72	0	4123	0449	0449	20	42.056	28.583	57.914	1.00	44.04	0
A104	4071	0447	0447	17	38.155	15.958	6.049	1.00	27.73	0	4124	0450	0450	20	15.434	52.096	27.975	1.00	39.94	0
A104	4072	0448	0448	17	32.659	22.367	51.695	1.00	36.96	0	4125	0451	0451	20	40.123	43.268	18.152	1.00	37.43	0
A104	4073	0449	0449	17	8.655	11.822	18.551	1.00	35.09	0	4126	0452	0452	20	14.301	18.529	21.331	1.00	32.32	0
A104	4074	0450	0450	18	61.442	16.332	49.671	1.00	27.27	0	4127	0453	0453	20	41.316	39.786	58.213	1.00	39.62	0
A104	4075	0451	0451	18	52.691	20.648	49.830	1.00	31.90	0	4128	0454	0454	20	28.167	15.941	46.987	1.00	39.62	0
A104	4076	0452	0452	18	22.398	9.094	32.744	1.00	46.70	0	4129	0455	0455	20	62.483	32.861	38.118	1.00	33.05	0
A104	4077	0453	0453	18	24.654	27.519	4.442	1.00	26.37	0	4130	0456	0456	20	50.420	44.042	41.952	1.00	24.33	0
A104	4078	0454	0454	18	26.112	52.226	27.595	1.00	38.43	0	4131	0457	0457	20	30.486	6.888	18.716	1.00	37.32	0
A104	4079	0455	0455	18	35.663	55.271	29.435	1.00	43.20	0	4132	0458	0458	20	39.000	11.315	44.273	1.00	38.40	0
A104	4080	0456	0456	18							4133	0459	0459	20						
A104	4081	0457	0457	18							4134	0460	0460	24						

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4135	041	041	X	24	26.342	44.842	18.030	1.00	27.39	8	4188	044	044	X	29	33.246	35.860	58.555	1.00	24.66	8
4136	042	042	X	24	42.233	42.967	22.516	1.00	28.16	8	4189	045	045	X	29	28.518	10.712	22.033	1.00	31.01	8
4137	043	043	X	24	17.859	41.857	40.950	1.00	44.87	8	4190	046	046	X	29	26.355	41.870	50.614	1.00	38.09	8
4138	044	044	X	24	18.776	45.302	34.594	1.00	36.85	8	4191	047	047	X	29	51.144	33.741	38.200	1.00	28.11	8
4139	045	045	X	24	17.339	48.385	29.218	1.00	36.40	8	4192	048	048	X	29	50.909	32.604	61.158	1.00	44.30	8
4140	046	046	X	24	59.859	17.628	38.947	1.00	24.80	8	4193	049	049	X	29	45.397	9.987	33.816	1.00	41.23	8
4141	047	047	X	24	44.716	26.845	15.361	1.00	31.66	8	4194	050	050	X	29	45.383	21.851	32.647	1.00	34.24	8
4142	048	048	X	24	16.851	22.367	25.144	1.00	38.33	8	4195	051	051	X	30	51.981	22.543	34.910	1.00	43.50	8
4143	049	049	X	24	44.428	18.344	31.454	1.00	28.97	8	4196	052	052	X	30	35.294	58.821	39.452	1.00	34.28	8
4144	050	050	X	25	51.824	36.690	57.769	1.00	27.33	8	4197	053	053	X	30	34.193	44.816	18.067	1.00	42.78	8
4145	051	051	X	25	53.680	40.328	57.339	1.00	34.91	8	4198	054	054	X	30	31.695	52.889	53.190	1.00	54.83	8
4146	052	052	X	25	46.573	15.118	12.832	1.00	38.80	8	4199	055	055	X	30	13.697	44.210	31.115	1.00	42.94	8
4147	053	053	X	25	29.409	35.711	7.581	1.00	30.09	8	4200	056	056	X	30	17.493	60.635	13.227	1.00	54.30	8
4148	054	054	X	25	26.515	13.237	3.213	1.00	30.52	8	4201	057	057	X	30	24.521	11.373	22.564	1.00	42.89	8
4149	055	055	X	25	20.273	3.147	8.139	1.00	29.22	8	4202	058	058	X	30	37.671	38.607	58.700	1.00	67.82	8
4150	056	056	X	25	34.516	42.011	19.433	1.00	23.40	8	4203	059	059	X	30	8.539	26.332	10.421	1.00	58.80	8
4151	057	057	X	25	41.463	52.238	24.452	1.00	33.83	8	4204	060	060	X	31	49.681	16.792	34.456	1.00	56.81	8
4152	058	058	X	25	18.346	37.804	42.302	1.00	35.93	8	4205	061	061	X	31	7.284	6.777	13.925	1.00	41.62	8
4153	059	059	X	25	35.243	54.671	32.179	1.00	58.94	8	4206	062	062	X	31	19.842	44.869	37.796	1.00	32.48	8
4154	060	060	X	26	44.229	16.673	16.585	1.00	37.25	8	4207	063	063	X	31	16.806	43.159	34.050	1.00	31.63	8
4155	061	061	X	26	44.766	14.121	14.499	1.00	46.53	8	4208	064	064	X	31	60.080	55.247	29.931	1.00	46.41	8
4156	062	062	X	26	31.390	33.920	59.134	1.00	33.03	8	4209	065	065	X	31	4.298	25.496	15.931	1.00	55.22	8
4157	063	063	X	26	12.971	21.397	23.449	1.00	37.89	8	4210	066	066	X	31	49.469	40.424	40.847	1.00	31.66	8
4158	064	064	X	26	41.239	11.310	51.389	1.00	40.81	8	4211	067	067	X	31	22.128	29.127	52.419	1.00	40.80	8
4159	065	065	X	26	41.929	11.632	42.697	1.00	45.17	8	4212	068	068	X	31	16.243	33.695	36.184	1.00	38.09	8
4160	066	066	X	26	42.707	44.751	57.570	1.00	42.32	8	4213	069	069	X	31	27.033	55.215	28.323	1.00	31.92	8
4161	067	067	X	26	56.463	33.749	51.681	1.00	36.66	8	4214	070	070	X	32	16.931	37.637	36.501	1.00	32.22	8
4162	068	068	X	26	24.821	11.342	3.728	1.00	31.27	8	4215	071	071	X	32	7.050	10.383	16.890	1.00	37.40	8
4163	069	069	X	26	60.493	39.175	53.713	1.00	47.98	8	4216	072	072	X	32	50.382	29.410	35.312	1.00	56.52	8
4164	070	070	X	27	45.625	38.306	11.910	1.00	37.28	8	4217	073	073	X	32	27.086	47.626	17.616	1.00	31.50	8
4165	071	071	X	27	43.803	49.874	24.898	1.00	75.50	8	4218	074	074	X	32	50.029	47.652	42.125	1.00	45.87	8
4166	072	072	X	27	28.316	2.149	14.607	1.00	42.07	8	4219	075	075	X	32	29.154	55.495	24.292	1.00	53.98	8
4167	073	073	X	27	52.604	30.867	37.880	1.00	33.10	8	4220	076	076	X	32	32.970	58.604	36.552	1.00	44.22	8
4168	074	074	X	27	55.458	34.651	38.180	1.00	47.45	8	4221	077	077	X	32	43.201	24.152	56.971	1.00	59.17	8
4169	075	075	X	27	49.808	19.847	34.189	1.00	33.89	8	4222	078	078	X	32	41.947	36.732	9.284	1.00	45.99	8
4170	076	076	X	27	1.703	6.632	4.199	1.00	62.88	8	4223	079	079	X	32	21.381	14.261	36.815	1.00	44.69	8
4171	077	077	X	27	48.275	39.555	43.586	1.00	28.38	8	4224	080	080	X	33	60.941	22.089	43.042	1.00	37.08	8
4172	078	078	X	27	23.975	20.226	6.003	1.00	41.62	8	4225	081	081	X	33	40.505	56.155	42.947	1.00	68.99	8
4173	079	079	X	27	59.679	43.247	57.111	1.00	53.07	8	4226	082	082	X	33	18.578	37.434	47.553	1.00	35.06	8
4174	080	080	X	28	21.533	51.639	33.545	1.00	49.86	8	4227	083	083	X	33	31.787	48.498	18.182	1.00	32.40	8
4175	081	081	X	28	1.544	11.851	5.024	1.00	69.29	8	4228	084	084	X	33	20.611	21.237	38.626	1.00	41.44	8
4176	082	082	X	28	23.566	45.229	15.525	1.00	28.33	8	4229	085	085	X	33	38.037	8.708	21.690	1.00	53.54	8
4177	083	083	X	28	44.831	57.241	34.859	1.00	42.49	8	4230	086	086	X	33	18.925	37.094	11.766	1.00	57.07	8
4178	084	084	X	28	33.378	9.541	42.581	1.00	51.32	8	4231	087	087	X	33	53.097	28.032	37.987	1.00	57.12	8
4179	085	085	X	28	27.186	6.024	0.021	1.00	46.35	8	4232	088	088	X	33	63.148	36.349	37.733	1.00	40.38	8
4180	086	086	X	28	56.162	41.254	59.120	1.00	56.59	8	4233	089	089	X	34	14.116	36.171	21.843	1.00	42.46	8
4181	087	087	X	28	5.756	19.201	7.132	1.00	20.05	8	4234	090	090	X	34	22.608	32.412	5.553	1.00	37.92	8
4182	088	088	X	28	14.700	29.886	48.603	1.00	35.67	8	4235	091	091	X	34	29.443	3.779	16.367	1.00	46.74	8
4183	089	089	X	28	41.585	56.275	32.373	1.00	42.13	8	4236	092	092	X	34	41.862	17.565	7.880	1.00	10.16	8
4184	090	090	X	29	24.984	49.494	43.922	1.00	40.12	8	4237	093	093	X	34	44.558	18.412	8.333	1.00	38.61	8
4185	091	091	X	29	29.979	22.421	2.045	1.00	42.88	8	4238	094	094	X	34	51.913	28.058	58.542	1.00	43.05	8
4186	092	092	X	29	18.885	13.752	26.566	1.00	49.31	8	4239	095	095	X	34	44.063	33.656	56.634	1.00	55.33	8
4187	093	093	X	29							4240	096	096	X	34	34.660	53.702	52.276	1.00	47.20	8

SUBSTITUTE SHEET (RULE 26)

ATOM	4241	008	001	X	34	5.844	14.713	12.911	1.00	40.12	0	17.196	19.679	22.863	1.00	53.81	0
ATOM	4242	009	001	X	34	19.697	54.257	50.395	1.00	36.68	0	22.069	3.918	3.047	1.00	55.02	0
ATOM	4243	000	001	X	35	18.706	24.537	40.234	1.00	51.89	0	40.725	28.659	11.393	1.00	42.74	0
ATOM	4244	001	001	X	35	20.209	21.570	34.426	1.00	34.23	0	53.521	31.821	60.008	1.00	46.58	0
ATOM	4245	002	001	X	35	44.584	17.646	26.801	1.00	35.48	0	43.778	45.011	23.702	1.00	52.91	0
ATOM	4246	003	001	X	35	41.430	32.246	57.799	1.00	36.05	0	45.725	48.904	38.294	1.00	35.75	0
ATOM	4247	004	001	X	35	13.266	6.166	0.033	1.00	49.40	0	49.126	11.559	46.679	1.00	49.02	0
ATOM	4248	005	001	X	35	42.162	53.175	26.887	1.00	43.15	0	68.137	39.801	42.467	1.00	64.82	0
ATOM	4249	006	001	X	35	33.503	56.216	55.522	1.00	56.63	0	19.785	19.132	28.386	1.00	38.16	0
ATOM	4250	007	001	X	35	1.397	8.422	6.422	1.00	48.68	0	46.799	34.048	27.779	1.00	51.88	0
ATOM	4251	008	001	X	35	47.778	11.987	38.953	1.00	34.48	0	46.195	38.407	29.718	1.00	67.17	0
ATOM	4252	009	001	X	35	15.856	27.767	43.683	1.00	55.40	0	18.791	46.608	27.796	1.00	36.46	0
ATOM	4253	000	001	X	36	38.734	7.626	16.829	1.00	43.46	0	17.255	25.962	28.182	1.00	49.71	0
ATOM	4254	001	001	X	36	10.578	1.426	2.281	1.00	40.52	0	38.815	10.903	18.927	1.00	48.73	0
ATOM	4255	002	001	X	36	50.000	33.981	35.051	1.00	49.14	0	47.017	51.069	47.161	1.00	58.10	0
ATOM	4256	003	001	X	36	44.622	34.879	33.356	1.00	60.84	0	52.558	36.860	39.163	1.00	51.88	0
ATOM	4257	004	001	X	36	3.816	18.327	21.655	1.00	80.04	0	19.024	23.922	31.261	1.00	60.30	0
ATOM	4258	005	001	X	36	41.431	56.503	45.767	1.00	53.22	0	55.428	38.709	38.776	1.00	50.63	0
ATOM	4259	006	001	X	36	49.548	26.317	22.816	1.00	58.00	0	23.391	20.916	45.898	1.00	44.61	0
ATOM	4260	007	001	X	36	37.549	29.346	4.956	1.00	52.92	0	6.072	14.391	18.394	1.00	42.40	0
ATOM	4261	008	001	X	36	49.240	44.486	55.149	1.00	38.00	0	42.371	37.835	9.565	1.00	46.80	0
ATOM	4262	009	001	X	36	53.734	18.532	52.601	1.00	51.95	0	6.020	13.163	15.876	1.00	60.89	0
ATOM	4263	000	001	X	37	39.041	11.166	25.698	1.00	36.59	0	2.465	17.737	5.335	1.00	44.54	0
ATOM	4264	001	001	X	37	10.532	4.916	16.271	1.00	58.74	0	39.431	8.272	34.832	1.00	46.23	0
ATOM	4265	002	001	X	37	41.366	7.373	32.768	1.00	47.04	0	43.239	42.742	20.441	1.00	42.07	0
ATOM	4266	003	001	X	37	32.474	41.914	15.484	1.00	44.27	0	43.667	29.039	33.074	1.00	53.81	0
ATOM	4267	004	001	X	37	18.592	28.534	17.648	1.00	41.36	0	22.754	6.724	-4.904	1.00	44.46	0
ATOM	4268	005	001	X	37	58.677	25.816	40.128	1.00	40.22	0	32.918	67.894	61.485	1.00	67.38	0
ATOM	4269	006	001	X	37	15.347	4.537	19.083	1.00	45.33	0	32.074	48.098	11.945	1.00	34.37	0
ATOM	4270	007	001	X	37	37.675	57.053	47.412	1.00	49.88	0	44.798	41.553	18.449	1.00	44.94	0
ATOM	4271	008	001	X	37	49.434	37.594	42.185	1.00	39.96	0	15.058	29.090	28.720	1.00	49.25	0
ATOM	4272	009	001	X	37	42.898	28.862	30.545	1.00	42.38	0	24.069	18.351	48.150	1.00	62.06	0
ATOM	4273	000	001	X	38	39.822	6.331	24.708	1.00	48.41	0	40.835	26.920	30.843	1.00	49.68	0
ATOM	4274	001	001	X	38	43.889	32.981	31.239	1.00	43.28	0	7.082	2.097	8.379	1.00	47.50	0
ATOM	4275	002	001	X	38	16.119	10.852	-3.221	1.00	34.08	0	47.039	51.990	40.775	1.00	51.23	0
ATOM	4276	003	001	X	38	46.051	14.381	33.005	1.00	54.04	0	22.252	13.968	43.293	1.00	38.13	0
ATOM	4277	004	001	X	38	26.251	44.941	50.891	1.00	58.57	0	23.106	31.488	52.711	1.00	57.06	0
ATOM	4278	005	001	X	38	41.308	26.375	9.990	1.00	50.76	0	23.054	7.691	20.407	1.00	52.15	0
ATOM	4279	006	001	X	38	51.350	42.087	41.209	1.00	49.03	0	21.526	1.631	11.156	1.00	53.95	0
ATOM	4280	007	001	X	38	38.215	7.892	30.920	1.00	43.67	0	20.140	18.123	39.073	1.00	62.86	0
ATOM	4281	008	001	X	38	22.827	33.878	7.842	1.00	43.67	0	17.481	51.997	31.031	1.00	80.00	0
ATOM	4282	009	001	X	39	69.722	41.667	12.969	1.00	47.74	0	46.380	42.021	59.675	1.00	51.50	0
ATOM	4283	000	001	X	39	35.999	18.255	51.330	1.00	59.07	0	33.452	41.508	56.803	1.00	58.62	0
ATOM	4284	001	001	X	39	43.974	10.373	31.316	1.00	53.37	0	47.654	43.632	31.945	1.00	43.18	0
ATOM	4285	002	001	X	39	33.924	10.373	31.316	1.00	53.37	0	26.231	12.181	43.880	1.00	49.95	0
ATOM	4286	003	001	X	39	22.588	10.397	39.495	1.00	42.79	0	14.968	36.024	33.676	1.00	63.17	0
ATOM	4287	004	001	X	39	19.514	48.906	21.847	1.00	68.43	0	62.986	20.054	42.528	1.00	50.37	0
ATOM	4288	005	001	X	39	13.468	27.723	5.713	1.00	66.89	0	45.852	21.374	58.053	1.00	55.98	0
ATOM	4289	006	001	X	39	45.654	25.542	43.943	1.00	44.03	0	50.564	43.538	16.798	1.00	34.34	0
ATOM	4290	007	001	X	39	44.078	13.029	36.846	1.00	57.57	0	35.077	40.600	13.082	1.00	45.23	0
ATOM	4291	008	001	X	39	27.240	0.087	12.390	1.00	48.13	0						
ATOM	4292	009	001	X	39	15.804	17.374	23.289	1.00	45.09	0						
ATOM	4293	000	001	X	40	21.294	12.036	34.534	1.00	58.48	0						
ATOM	4294	001	001	X	40	47.490	44.003	18.045	1.00	60.75	0						

AT04	4367	045	045	1.00	41.94	1.00	41.94	8	8	43.751	9.508	10.207	1.00	72.09	8
AT04	4368	046	046	1.00	43.14	1.00	43.14	8	8	21.156	18.175	-5.366	1.00	59.35	8
AT04	4369	047	047	1.00	44.28	1.00	44.28	8	8	28.822	20.591	38.525	1.00	53.15	8
AT04	4370	048	048	1.00	45.42	1.00	45.42	8	8	25.847	41.728	50.223	1.00	53.16	8
AT04	4371	049	049	1.00	46.56	1.00	46.56	8	8	42.406	49.580	54.444	1.00	49.42	8
AT04	4372	050	050	1.00	47.70	1.00	47.70	8	8	11.152	-0.896	4.529	1.00	73.12	8
AT04	4373	051	051	1.00	48.84	1.00	48.84	8	8	41.064	10.519	39.198	1.00	74.33	8
AT04	4374	052	052	1.00	49.98	1.00	49.98	8	8	11.838	45.452	24.174	1.00	52.20	8
AT04	4375	053	053	1.00	51.12	1.00	51.12	8	8	24.803	8.582	38.134	1.00	48.46	8
AT04	4376	054	054	1.00	52.26	1.00	52.26	8	8	28.241	55.029	32.933	1.00	56.81	8
AT04	4377	055	055	1.00	53.40	1.00	53.40	8	8	26.326	46.042	48.362	1.00	42.89	8
AT04	4378	056	056	1.00	54.54	1.00	54.54	8	8	60.372	23.243	57.581	1.00	51.46	8
AT04	4379	057	057	1.00	55.68	1.00	55.68	8	8	44.063	13.169	3.195	1.00	73.23	8
AT04	4380	058	058	1.00	56.82	1.00	56.82	8	8	29.959	38.273	7.993	1.00	74.56	8
AT04	4381	059	059	1.00	57.96	1.00	57.96	8	8	17.959	47.341	32.823	1.00	52.58	8
AT04	4382	060	060	1.00	59.10	1.00	59.10	8	8	35.761	36.887	7.808	1.00	46.76	8
AT04	4383	061	061	1.00	60.24	1.00	60.24	8	8	29.185	14.140	50.554	1.00	100.00	8
AT04	4384	062	062	1.00	61.38	1.00	61.38	8	8	46.852	47.489	54.235	1.00	47.47	8
AT04	4385	063	063	1.00	62.52	1.00	62.52	8	8	66.126	18.871	10.000	1.00	74.45	8
AT04	4386	064	064	1.00	63.66	1.00	63.66	8	8	43.487	42.127	14.225	1.00	58.79	8
AT04	4387	065	065	1.00	64.80	1.00	64.80	8	8	42.354	10.824	26.570	1.00	74.16	8
AT04	4388	066	066	1.00	65.94	1.00	65.94	8	8	61.382	9.160	28.416	1.00	65.06	8
AT04	4389	067	067	1.00	67.08	1.00	67.08	8	8	32.269	16.276	51.085	1.00	66.53	8
AT04	4390	068	068	1.00	68.22	1.00	68.22	8	8	43.754	20.935	55.297	1.00	89.21	8
AT04	4391	069	069	1.00	69.36	1.00	69.36	8	8	66.525	23.435	61.833	1.00	64.40	8
AT04	4392	070	070	1.00	70.50	1.00	70.50	8	8	38.689	9.501	46.403	1.00	43.78	8
AT04	4393	071	071	1.00	71.64	1.00	71.64	8	8	13.785	14.234	21.394	1.00	46.49	8
AT04	4394	072	072	1.00	72.78	1.00	72.78	8	8	44.108	8.308	6.121	1.00	74.38	8
AT04	4395	073	073	1.00	73.92	1.00	73.92	8	8	37.095	13.297	47.553	1.00	92.89	8
AT04	4396	074	074	1.00	75.06	1.00	75.06	8	8	60.232	38.361	56.675	1.00	71.18	8
AT04	4397	075	075	1.00	76.20	1.00	76.20	8	8	43.876	52.184	52.067	1.00	52.01	8
AT04	4398	076	076	1.00	77.34	1.00	77.34	8	8	13.472	21.519	26.526	1.00	85.06	8
AT04	4399	077	077	1.00	78.48	1.00	78.48	8	8	26.573	48.774	55.261	1.00	63.24	8
AT04	4400	078	078	1.00	79.62	1.00	79.62	8	8	38.373	54.855	25.877	1.00	61.51	8
AT04	4401	079	079	1.00	80.76	1.00	80.76	8	8	40.109	29.094	7.323	1.00	50.88	8
AT04	4402	080	080	1.00	81.90	1.00	81.90	8	8	40.897	28.288	33.474	1.00	55.10	8
AT04	4403	081	081	1.00	83.04	1.00	83.04	8	8	26.559	57.407	32.671	1.00	74.31	8
AT04	4404	082	082	1.00	84.18	1.00	84.18	8	8	15.383	36.894	33.336	1.00	63.49	8
AT04	4405	083	083	1.00	85.32	1.00	85.32	8	8	25.837	23.924	51.791	1.00	62.36	8
AT04	4406	084	084	1.00	86.46	1.00	86.46	8	8	47.868	37.197	21.724	1.00	98.01	8
AT04	4407	085	085	1.00	87.60	1.00	87.60	8	8	48.664	28.592	20.875	1.00	61.42	8
AT04	4408	086	086	1.00	88.74	1.00	88.74	8	8	22.182	11.543	42.558	1.00	50.93	8
AT04	4409	087	087	1.00	89.88	1.00	89.88	8	8	14.290	33.767	23.519	1.00	43.45	8
AT04	4410	088	088	1.00	91.02	1.00	91.02	8	8	49.254	21.261	57.308	1.00	74.77	8
AT04	4411	089	089	1.00	92.16	1.00	92.16	8	8	32.872	50.437	56.442	1.00	84.60	8
AT04	4412	090	090	1.00	93.30	1.00	93.30	8	8	6.861	26.478	7.012	1.00	89.24	8
AT04	4413	091	091	1.00	94.44	1.00	94.44	8	8	36.069	6.771	2.277	1.00	89.64	8
AT04	4414	092	092	1.00	95.58	1.00	95.58	8	8	60.239	29.387	37.677	1.00	64.46	8
AT04	4415	093	093	1.00	96.72	1.00	96.72	8	8	46.693	15.500	46.504	1.00	37.40	8
AT04	4416	094	094	1.00	97.86	1.00	97.86	8	8	47.685	47.802	26.981	1.00	44.40	8
AT04	4417	095	095	1.00	99.00	1.00	99.00	8	8	21.472	47.007	15.910	1.00	70.01	8
AT04	4418	096	096	1.00	100.14	1.00	100.14	8	8	2.967	21.682	3.603	1.00	80.74	8
AT04	4419	097	097	1.00	101.28	1.00	101.28	8	8	62.723	25.567	58.195	1.00	45.51	8

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AT04	4559	043	041	X	70	12.149	0.500	-0.175	1.00100.00	8	AT04	4612	042	041	X	81	33.361	34.872	36.349	1.00 64.66	8
AT04	4560	044	041	X	70	24.781	48.147	16.489	1.00 53.74	8	AT04	4613	043	041	X	81	51.628	42.754	59.455	1.00 87.45	8
AT04	4561	045	041	X	70	45.295	18.429	15.166	1.00 64.52	8	AT04	4614	045	041	X	81	17.748	48.786	43.576	1.00 81.62	8
AT04	4562	046	041	X	70	16.273	24.172	43.929	1.00 86.28	8	AT04	4615	046	041	X	81	40.981	31.297	32.687	1.00 92.90	8
AT04	4563	047	041	X	71	14.692	0.299	4.588	1.00 76.24	8	AT04	4616	047	041	X	81	36.339	42.304	57.906	1.00 54.44	8
AT04	4564	048	041	X	71	56.655	45.988	66.463	1.00 74.53	8	AT04	4617	048	041	X	82	52.150	44.557	55.907	1.00 81.29	8
AT04	4565	049	041	X	71	46.653	15.572	21.588	1.00 81.92	8	AT04	4618	049	041	X	82	44.696	27.699	29.800	1.00 68.84	8
AT04	4566	050	041	X	71	13.915	34.012	32.549	1.00 76.95	8	AT04	4619	050	041	X	82	15.349	42.073	36.641	1.00 87.69	8
AT04	4567	051	041	X	72	18.894	23.324	28.037	1.00 89.01	8	AT04	4620	051	041	X	82	44.262	38.613	61.725	1.00 74.79	8
AT04	4568	052	041	X	72	25.942	27.528	52.388	1.00 80.30	8	AT04	4621	052	041	X	82	10.687	37.555	22.160	1.00 77.71	8
AT04	4569	053	041	X	72	20.444	43.760	44.743	1.00 57.92	8	AT04	4622	053	041	X	82	57.317	26.895	38.482	1.00 54.04	8
AT04	4570	054	041	X	72	56.463	15.927	54.362	1.00 90.66	8	AT04	4623	054	041	X	83	1.485	10.546	14.639	1.00 49.60	8
AT04	4571	055	041	X	72	67.258	38.530	48.388	1.00 67.91	8	AT04	4624	055	041	X	83	44.383	11.585	44.954	1.00 89.75	8
AT04	4572	056	041	X	73	13.119	23.916	-2.569	1.00 57.58	8	AT04	4625	056	041	X	83	13.091	19.090	23.540	1.00 84.10	8
AT04	4573	057	041	X	73	27.753	4.319	2.523	1.00 68.14	8	AT04	4626	057	041	X	83	49.644	18.609	50.424	1.00 79.36	8
AT04	4574	058	041	X	73	15.049	27.612	26.948	1.00 71.05	8	AT04	4627	058	041	X	83	-0.411	-0.186	6.219	1.00 73.91	8
AT04	4575	059	041	X	73	41.506	30.331	28.071	1.00 39.96	8	AT04	4628	059	041	X	84	-0.060	12.467	10.762	1.00 74.36	8
AT04	4576	060	041	X	73	49.356	13.175	50.180	1.00 77.21	8	AT04	4629	060	041	X	84	45.916	18.172	53.625	1.00 82.88	8
AT04	4577	061	041	X	74	44.776	9.064	36.247	1.00 56.22	8	AT04	4630	061	041	X	84	42.886	23.516	61.123	1.00 71.70	8
AT04	4578	062	041	X	74	14.995	33.147	12.393	1.00 74.77	8	AT04	4631	062	041	X	84	26.711	5.741	19.232	1.00 65.61	8
AT04	4579	063	041	X	74	21.394	18.527	43.796	1.00 77.10	8	AT04	4632	063	041	X	84	18.341	21.188	47.071	1.00 79.82	8
AT04	4580	064	041	X	74	32.705	3.566	1.290	1.00 100.00	8	AT04	4633	064	041	X	85	45.303	21.545	29.439	1.00 65.08	8
AT04	4581	065	041	X	74	23.871	44.907	16.023	1.00 71.10	8	AT04	4634	065	041	X	85	47.617	21.423	28.329	1.00 72.90	8
AT04	4582	066	041	X	74	41.289	9.005	3.932	1.00 11.97	8	AT04	4635	066	041	X	85	14.724	8.133	-4.054	1.00 80.41	8
AT04	4583	067	041	X	75	38.329	57.673	44.241	1.00 64.90	8	AT04	4636	067	041	X	85	16.404	38.980	34.440	1.00 73.60	8
AT04	4584	068	041	X	75	18.910	30.950	52.593	1.00 86.30	8	AT04	4637	068	041	X	85	38.711	59.411	56.032	1.00 72.07	8
AT04	4585	069	041	X	75	68.020	16.610	50.288	1.00 86.49	8	AT04	4638	069	041	X	86	30.350	51.931	56.463	1.00 83.08	8
AT04	4586	070	041	X	75	22.139	39.199	7.275	1.00 71.53	8	AT04	4639	070	041	X	86	28.737	50.755	56.620	1.00 78.91	8
AT04	4587	071	041	X	76	58.720	42.672	38.660	1.00 88.73	8	AT04	4640	071	041	X	86	38.447	9.203	1.111	1.00 60.02	8
AT04	4588	072	041	X	76	61.482	44.540	47.192	1.00 77.48	8	AT04	4641	072	041	X	86	63.955	18.750	55.290	1.00 75.30	8
AT04	4589	073	041	X	76	22.107	41.072	47.776	1.00 60.73	8	AT04	4642	073	041	X	86	28.437	41.435	56.329	1.00 77.99	8
AT04	4590	074	041	X	76	2.634	-1.318	3.949	1.00 69.94	8	AT04	4643	074	041	X	86	27.951	49.707	19.814	1.00 80.65	8
AT04	4591	075	041	X	77	32.187	5.643	25.223	1.00 76.13	8	AT04	4644	075	041	X	86	33.978	8.299	40.249	1.00 69.22	8
AT04	4592	076	041	X	77	67.602	33.866	51.363	1.00 72.25	8	AT04	4645	076	041	X	86	17.498	1.898	10.616	1.00 71.37	8
AT04	4593	077	041	X	77	52.748	50.627	48.547	1.00 74.39	8	AT04	4646	077	041	X	87	1.270	35.798	6.438	1.00 70.87	8
AT04	4594	078	041	X	77	10.304	44.509	26.769	1.00 64.94	8	AT04	4647	078	041	X	87	37.174	55.549	52.513	1.00 69.91	8
AT04	4595	079	041	X	77	22.754	10.234	24.846	1.00 66.60	8	AT04	4648	079	041	X	87	68.146	21.847	55.397	1.00 70.79	8
AT04	4596	080	041	X	78	65.372	34.387	54.026	1.00 88.26	8	AT04	4649	080	041	X	87	24.655	52.548	24.459	1.00 72.31	8
AT04	4597	081	041	X	78	61.952	23.010	40.260	1.00 64.64	8	AT04	4650	081	041	X	87	48.009	24.986	33.287	1.00 79.82	8
AT04	4598	082	041	X	78	6.141	-0.725	8.920	1.00 63.43	8	AT04	4651	082	041	X	87	50.195	14.529	36.835	1.00 65.15	8
AT04	4599	083	041	X	78	62.946	40.127	37.159	1.00 74.43	8	AT04	4652	083	041	X	87	39.201	3.240	-2.272	1.00 78.74	8
AT04	4600	084	041	X	79	57.524	45.787	43.333	1.00 68.47	8	AT04	4653	084	041	X	88	13.357	32.018	24.857	1.00 62.05	8
AT04	4601	085	041	X	79	27.601	6.844	22.548	1.00 100.00	8	AT04	4654	085	041	X	88	45.406	20.886	50.995	1.00 76.49	8
AT04	4602	086	041	X	79	31.772	31.115	20.743	1.00 57.33	8	AT04	4655	086	041	X	88	20.515	8.228	19.759	1.00 73.98	8
AT04	4603	087	041	X	79	58.663	33.880	36.310	1.00 71.62	8	AT04	4656	087	041	X	88	46.758	18.587	30.455	1.00 74.75	8
AT04	4604	088	041	X	79	49.511	45.784	34.237	1.00 64.41	8	AT04	4657	088	041	X	88	49.679	43.124	20.624	1.00 80.84	8
AT04	4605	089	041	X	80	64.430	34.390	57.479	1.00 81.60	8	AT04	4658	089	041	X	89	60.303	44.435	40.737	1.00 70.62	8
AT04	4606	090	041	X	80	51.348	32.222	4.650	1.00 86.83	8	AT04	4659	090	041	X	89	13.248	-1.159	9.184	1.00 78.53	8
AT04	4607	091	041	X	80	28.165	77.493	33.768	1.00 71.08	8	AT04	4660	091	041	X	89	61.708	19.538	53.061	1.00 64.93	8
AT04	4608	092	041	X	80	45.757	27.493	53.748	1.00 48.10	8	AT04	4661	092	041	X	89	24.291	28.301	8.472	1.00 69.88	8
AT04	4609	093	041	X	80	45.249	12.674	37.874	1.00 50.64	8	AT04	4662	093	041	X	89	27.964	24.098	-2.600	1.00 66.61	8
AT04	4610	094	041	X	81						AT04	4663	094	041	X	90	22.140	24.413	52.912	1.00 67.47	8

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A104	6655	043	041	X	90	39.112	6.740	5.854	1.00	66.72	0
A104	6656	044	041	X	90	43.164	57.893	49.964	1.00	71.30	0
A104	6657	045	041	X	90	16.187	17.842	27.844	1.00	71.83	0
A104	6658	047	041	X	90	22.913	3.223	6.101	1.00	63.34	0
A104	6659	040	041	X	91	0.373	23.417	18.664	1.00	68.95	0
A104	6670	041	041	X	91	19.144	22.297	52.147	1.00	68.45	0
A104	6671	042	041	X	91	46.750	22.374	17.228	1.00	68.56	0
A104	6672	043	041	X	91	50.310	39.246	9.155	1.00	68.48	0
A104	6673	045	041	X	91	14.832	31.811	-1.674	1.00	65.32	0
A104	6674	046	041	X	91	39.548	22.971	59.602	1.00	94.75	0
A104	6675	040	041	X	92	28.305	37.474	53.688	1.00	64.82	0
A104	6676	041	041	X	92	60.842	35.837	35.557	1.00	68.20	0
A104	6677	043	041	X	92	38.306	2.043	9.940	1.00	74.71	0
A104	6678	044	041	X	92	37.932	10.810	23.873	1.00	62.54	0
A104	6679	045	041	X	92	37.872	59.284	31.500	1.00	64.40	0
A104	6680	048	041	X	92	16.587	37.900	45.458	1.00	57.48	0
A104	6681	042	041	X	93	24.426	6.991	31.459	1.00	62.04	0
A104	6682	043	041	X	93	15.322	46.823	24.885	1.00	68.48	0
A104	6683	045	041	X	93	18.754	23.194	42.946	1.00	69.72	0
A104	6684	046	041	X	93	20.937	44.805	43.439	1.00	65.25	0
A104	6685	048	041	X	93	28.767	42.761	53.085	1.00	51.35	0
A104	6686	040	041	X	94	32.517	16.473	33.381	1.00	60.16	0
A104	6687	042	041	X	94	26.635	4.800	29.351	1.00	63.33	0
A104	6688	043	041	X	94	1.194	4.216	9.172	1.00	60.34	0
A104	6689	044	041	X	94	25.652	19.885	-5.299	1.00	58.09	0
A104	6690	045	041	X	94	43.661	12.692	20.184	1.00	65.23	0
A104	6691	046	041	X	94	17.439	46.586	41.518	1.00	64.21	0
A104	6692	047	041	X	94	35.133	15.687	30.639	1.00	49.75	0
A104	6693	048	041	X	94	38.346	8.698	18.844	1.00	48.58	0
A104	6694	040	041	X	95	30.818	8.165	40.656	1.00	54.86	0
A104	6695	041	041	X	95	40.089	21.776	55.785	1.00	53.69	0
A104	6696	042	041	X	95	18.639	14.065	-5.612	1.00	55.94	0
A104	6697	043	041	X	95	51.587	38.457	41.331	1.00	54.04	0
A104	6698	044	041	X	95	50.107	29.481	17.255	1.00	56.08	0
A104	6699	046	041	X	95	8.218	14.744	20.596	1.00	56.95	0
A104	6700	046	041	X	95	40.674	47.760	57.927	1.00	54.91	0

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CLAIMS

1. A method of constructing a variant of a parent Termamyl-like α -amylase, which variant has α -amylase activity and at least one altered property as compared to said parent α -amylase, which method comprises

i) analysing the structure of the parent Termamyl-like α -amylase to identify at least one amino acid residue or at least one structural part of the Termamyl-like α -amylase structure, which amino acid residue or structural part is believed to be of relevance for altering said property of the parent Termamyl-like α -amylase (as evaluated on the basis of structural or functional considerations),

ii) constructing a Termamyl-like α -amylase variant, which as compared to the parent Termamyl-like α -amylase, has been modified in the amino acid residue or structural part identified in i) so as to alter said property, and

iii) testing the resulting Termamyl-like α -amylase variant for said property.

2. The method according to claim 1, wherein the property to be altered is selected from the group consisting of substrate specificity, substrate binding, substrate cleavage pattern, temperature stability, pH dependent activity, pH dependent stability (especially increased stability at low (e.g. pH<6) or high (e.g. pH>9) pH values), stability towards oxidation, Ca^{2+} -dependency and specific activity.

3. The method according to claim 1 or 2, wherein the property to be altered is the calcium ion dependency and the structural part to be modified is selected from the group consisting of the C domain, the interface between the A and B domain, the interface between the A and C domain, or the interaction to a calcium binding site of the Termamyl-like α -amylase.

4. The method according to claim 1 or 2, wherein the property to be altered is the substrate cleavage pattern and the structural part to be modified is located within 10Å from an amino acid residue of the substrate binding site.

5

5. A method of constructing a variant of a parent Termamyl-like α -amylase, which variant has α -amylase activity and one or more altered properties as compared to said parent α -amylase, which method comprises

10 i) comparing the three-dimensional structure of the Termamyl-like α -amylase with the structure of a non-Termamyl-like α -amylase,

ii) identifying a part of the Termamyl-like α -amylase structure which is different from the non-Termamyl-like α -amylase
15 structure and which from structural or functional considerations is contemplated to be responsible for differences in one or more properties of the Termamyl-like and non-Termamyl-like α -amylase, and

iii) modifying the part of the Termamyl-like α -amylase
20 identified in ii) whereby a Termamyl-like α -amylase variant is obtained, one or more properties of which differ from the parent Termamyl-like α -amylase.

6. The method according to claim 6, wherein, in step iii), the
25 part of the Termamyl-like α -amylase is modified so as to resemble the corresponding part of the non-Termamyl-like α -amylase.

7. The method according to claim 5 or 6, wherein, in step iii),
30 the modification is accomplished by deleting one or more amino acid residues of the part of the Termamyl-like α -amylase to be modified; by replacing one or more amino acid residues of the part of the Termamyl-like α -amylase to be modified with the amino acid residues occupying corresponding positions in the
35 non-Termamyl-like α -amylase; or by insertion of one or more amino acid residues present in the non-Termamyl-like α -amylase into a corresponding position in the Termamyl-like α -amylase.

8. The method according to any of claims 5-7, wherein the non-Termamyl-like α -amylase structure is the structure of a fungal α -amylase or a mammalian α -amylase.

5 9. The method according to claim 8, wherein the non-Termamyl-like α -amylase is the *Aspergillus oryzae* TAKA α -amylase, the *A. niger* acid α -amylase, the *Bacillus subtilis* α -amylase or the pig pancreatic α -amylase.

10 10. The method according to any of claims 1-9, wherein the parent Termamyl-like α -amylase is derived from a strain of *Bacillus*.

11. The method according to claim 10, wherein the parent α -
15 amylase is derived from a strain of a *B. licheniformis*, *B. amyloliquefaciens*, *B. stearothermophilus* or a strain from an alkalophilic *Bacillus* sp. such as NCIB 12289, NCIB 12512 or NCIB 12513.

20 12. The method according to any of claims 1-11, wherein the parent α -amylase is a hybrid α -amylase comprising a combination of partial amino acid sequences derived from at least two α -amylases, of which one is a Termamyl-like α -amylase and the other(s) are, e.g., from a microbial and/or a mammalian α -
25 amylase.

13. The method according to any of claims 5-12, wherein the part of the parent Termamyl-like α -amylase to be modified and identified in step ii) is loop 1, loop 2, loop 3 and/or loop 8
30 of the parent α -amylase.

13. A method of constructing a variant of a parent Termamyl-like α -amylase, which has a decreased calcium ion dependency as compared to said parent, which method comprises:

35

i) identifying an amino acid residue within 10Å from a Ca^{2+} binding site of a Termamyl-like α -amylase in a model of the three-dimensional structure of said α -amylase, which from

structural or functional considerations is believed to be responsible for a non-optimal calcium ion interaction,

- ii) constructing a variant in which said amino acid residue is replaced with another amino acid residue which from structural or functional considerations is believed to be important for establishing a higher Ca^{2+} binding affinity, and
- iii) testing the Ca^{2+} dependency of the resulting Termamyl-like α -amylase variant.

10 14. A method of constructing a variant of a parent Termamyl-like α -amylase which variant has α -amylase activity and an altered pH dependent activity, which method comprises

- i) in a three-dimensional structure of the Termamyl-like α -
15 amylase in question, identifying an amino acid residue within 15Å from an active site residue, in particular 10Å from an active site residue, which amino acid residue is contemplated to be involved in electrostatic or hydrophobic interactions with an active site residue,

20

- ii) replacing, in the structure, said amino acid residue with an amino acid residue which changes the electrostatic and/or hydrophobic surroundings of an active site residue and evaluating the accomodation of the amino acid residue in the
25 structure,

- iii) optionally repeating step i) and/or ii) until an amino acid replacement has been identified which is accomodated into the structure,

30

- iv) constructing a Termamyl-like α -amylase variant resulting from steps i), ii) and optionally iii) and testing the pH dependent activity of said variant.

35 15. A method of increasing the thermostability and/or altering the temperature optimum of a parent Termamyl-like α -amylase, which method comprises

- i) identifying an internal hole or a crevice of the parent Termamyl-like α -amylase in the three-dimensional structure of said α -amylase,
- ii) replacing, in the structure, one or more amino acid residues in the neighbourhood of the hole or crevice identified in i) with another amino acid residue which from structural or functional considerations is believed to increase the hydrophobic interaction and to fill out or reduce the size of the hole or crevice,
- 10 iii) constructing a Termamyl-like α -amylase variant resulting from step ii) and testing the thermostability and/or temperature optimum of the variant.

16. A method of constructing a variant of a Termamyl-like α -amylase which has a reduced ability to cleave a substrate close to the branching point, which method comprises

- i) identifying the substrate binding area of the parent Termamyl-like α -amylase in a model of the three-dimensional structure of said α -amylase,
- 20 ii) replacing, in the model, one or more amino acid residues of the substrate binding area of the cleft identified in i), which is/are believed to be responsible for the cleavage pattern of the parent α -amylase, with another amino acid residue which from structural considerations is believed to result in an altered substrate cleavage pattern, or deleting one or more amino acid residues of the substrate binding area contemplated to introduce favourable interactions to the substrate or adding
- 30 one or more amino acid residues to the substrate binding area contemplated to introduce favourable interactions to the substrate, and
- iii) constructing a Termamyl-like α -amylase variant resulting from step ii) and testing the substrate cleavage pattern of the
- 35 variant.

17. The method according to any of the preceding claims, in which the α -amylase variant is obtained by cultivating a

microorganism comprising a DNA sequence encoding the variant under conditions which are conducive for producing the variant, and optionally subsequently recovering the variant from the resulting culture broth.

5

18. A variant of a parent Termamyl-like α -amylase, in which variant at least one amino acid residue of the parent α -amylase, which is/are present in a fragment corresponding to the amino acid fragment 44-57 of the amino acid sequence of SEQ
10 ID No. 4, has been deleted or replaced with one or more amino acid residues which is/are present in a fragment corresponding to the amino acid fragment 66-84 of the amino acid sequence shown in SEQ ID No. 10, or in which one or more additional amino acid residues has been added using the relevant part of
15 SEQ ID No. 10 or a corresponding part of another Fungamyl-like α -amylase as a template.

19. A variant of a parent Termamyl-like α -amylase, which variant has a region which, when the amino acid sequence of
20 variant is aligned most closely with the amino acid sequence of the said parent α -amylase, occupies the same position as the portion from residue X to residue Y of SEQ ID No 4, the said region having at least 80% sequence homology with the part of SEQ ID No 10 extending from residue Z to residue V of SEQ ID No
25 10, wherein

X is the amino acid residue occupying position 44, 45, 46, 47 or 48 of SEQ ID No. 4,

Y is the amino acid residue occupying position 51, 52, 53, 54, 55, 56 or 57 of SEQ ID No. 4,

30 Z is the amino acid residue occupying position 66, 67, 68, 69 or 70 of SEQ ID No. 10, and

V is the amino acid residue occupying position 78, 79, 80, 81, 82, 83 or 84 of SEQ ID No. 10.

35 20. The variant according to claim 18 or 19, wherein X is the amino acid residue occupying position 48 and Y the amino acid residue occupying position 51 of SEQ ID NO 4 and Z is the amino

acid residue occupying position 70 and V the amino acid residue occupying position 78 in SEQ ID No 10.

21. A variant of a parent Termamyl-like α -amylase, in which
5 variant at least one of the amino acid residues of the parent
 α -amylase, which is/are present in an amino acid fragment
corresponding to the amino acid fragment 195-202 of the amino
acid sequence of SEQ ID No. 4, has been deleted or replaced
with one or more of the amino acid residues which is/are
10 present in an amino acid fragment corresponding to the amino
acid fragment 165-177 of the amino acid sequence shown in SEQ
ID No. 10, or in which one or more additional amino acid
residues has been added using the relevant part of SEQ ID No.
10 or a corresponding part of another Fungamyl-like α -amylase
15 as a template.

22. A variant of a parent Termamyl-like α -amylase, which
variant has a region which, when the amino acid sequence of
variant is aligned most closely with the amino acid sequence of
20 the said parent α -amylase, occupies the same position as the
portion from residue X to residue Y of SEQ ID No 4, the said
region having at least 80%, such as 90% sequence homology with
the part of SEQ ID No 10 extending from residue Z to residue V
of SEQ ID No 10, wherein
25 X is the amino acid occupying position 195 or 196 of SEQ ID No.
4,

Y is the amino acid residue occupying position 198, 199, 200,
201, or 202 of SEQ ID No. 4,

30

Z is the amino acid residue occupying position 165 or 166 of
SEQ ID No. 10, and

V is the amino acid residue occupying position 173, 174, 175,
35 176 or 177 of SEQ ID No. 10.

23. The variant according to claim 21 or 22, in which the amino
acid fragment of the parent α -amylase, which corresponds to

amino acid residues 196-198 of SEQ ID No. 4, has been replaced with the amino acid fragment corresponding to amino acid residues 166-173 of the amino acid sequence shown in SEQ ID No. 10.

5

24. A variant of a parent Termamyl-like α -amylase, in which variant at least one of the amino acid residues of the parent α -amylase, which is/are present in a fragment corresponding to the amino acid fragment 117-185 of the amino acid sequence of
10 SEQ ID No. 4, has/have been deleted or replaced with one or more of the amino acid residues, which is/are present in an amino acid fragment corresponding to the amino acid fragment 98-210 of the amino acid sequence shown in SEQ ID No. 10, or in which one or more additional amino acid residues has been added
15 using the relevant part of SEQ ID No. 10 or a corresponding part of another Fungamyl-like α -amylase as a template.

25. A variant of a parent Termamyl-like α -amylase, which variant has a region which, when the amino acid sequence of
20 variant is aligned most closely with the amino acid sequence of the said parent α -amylase, occupies the same position as the portion from residue X to residue Y of SEQ ID No 4, the said region having at least 80%, such as at least 90% sequence homology with the part of SEQ ID No 10 extending from residue
25 Z to residue V of SEQ ID No 10, wherein

X is the amino acid occupying position 117, 118, 119, 120 or 121 of SEQ ID No. 4,

30 Y is the amino acid occupying position 181, 182, 183, 184 or 185 of SEQ ID No. 4,

Z is the amino acid occupying position 98, 99, 100, 101, 102 of SEQ ID No. 10, and

35

V is the amino acid occupying position 206, 207, 208, 209 or 210 of SEQ ID No. 10.

26. The variant according to claim 24 or 25, in which an amino acid fragment of the parent α -amylase, which corresponds to amino acid residues 121-181 of SEQ ID No. 4, has been replaced with the amino acid fragment corresponding to amino acid residues 102-206 of the amino acid sequence shown in SEQ ID No. 10.

27. A variant of a parent Termamyl-like α -amylase, in which variant at least one of the amino acid residues of the parent α -amylase, which is/are present in a fragment corresponding to the amino acid fragment 117-181 of the amino acid sequence of SEQ ID No. 4, has/have been deleted or replaced with one or more of the amino acid residues, which is/are present in an amino acid fragment corresponding to the amino acid fragment to 98-206 of the amino acid sequence shown in SEQ ID No. 10, or in which one or more additional amino acid residues has been added using the relevant part of SEQ ID No. 10 or a corresponding part of another Fungamyl-like α -amylase as a template.

20

28. A variant of a parent Termamyl-like α -amylase, which variant has a region which, when the amino acid sequence of variant is aligned most closely with the amino acid sequence of the said parent α -amylase, occupies the same position as the portion from residue X to residue Y of SEQ ID No 4, the said region having at least 80%, such as at least 90% sequence homology with the part of SEQ ID No 10 extending from residue Z to residue V of SEQ ID No 10, wherein X is the amino acid occupying position 117, 118, 119, 120 or 121 of SEQ ID No. 4,

Y is the amino acid occupying position 174, 175, 176 or 177 of SEQ ID No. 4,

Z is the amino acid occupying position 98, 99, 100, 101, 102 of SEQ ID No. 10, and

V is the amino acid occupying position 199, 200, 201 or 202 of SEQ ID No. 10.

29. The variant according to claim 27 or 28, in which the amino acid fragment of the parent α -amylase, which corresponds to amino acid residues 121-174 of SEQ ID No. 4, has been replaced with the amino acid fragment corresponding to amino acid residues 102-199 of the amino acid sequence shown in SEQ ID No. 10.

10

30. A variant of a parent Termamyl-like α -amylase, in which variant at least one of the amino acid residues of the parent α -amylase, which is/are present in an amino acid fragment corresponding to the amino acid fragment 12-19 of the amino acid sequence of SEQ ID No. 4, has/have been deleted or replaced with one or more of the amino acid residues, which is/are present in an amino acid fragment which corresponds to the amino acid fragment 28-42 of SEQ ID No. 10, or in which one or more additional amino acid residues has/have been inserted using the relevant part of SEQ ID No. 10 or a corresponding part of another Fungamyl-like α -amylase as a template.

31. A variant of a parent Termamyl-like α -amylase, which variant has a region which, when the amino acid sequence of variant is aligned most closely with the amino acid sequence of the said parent α -amylase, occupies the same position as the portion from residue X to residue Y of SEQ ID No 4, the said region having at least 80%, such as at least 90% sequence homology with the part of SEQ ID No 10 extending from residue Z to residue V of SEQ ID No 10, wherein

X is the amino acid occupying position 12, 13 or 14 of SEQ ID No. 4,

Y is the amino acid occupying position 15, 16, 17, 18 or 19 of SEQ ID No. 4,

35 Z is the amino acid occupying position 28, 29, 30, 31 or 32 of SEQ ID No. 10, and

V is an amino acid residue corresponding to the amino acid occupying position 38, 39, 40, 41 or 42 of SEQ ID No. 10.

32. The variant according to claim 30 or 31, in which the amino acid fragment of the parent α -amylase, which corresponds to amino acid residues 14-15 of SEQ ID No. 4, has been replaced with the amino acid fragment corresponding to amino acid residues 32-38 of the amino acid sequence shown in SEQ ID No. 10.

33. A variant of a parent Termamyl-like α -amylase, in which variant at least one of the amino acid residues of the parent
10 α -amylase, which is present in a fragment corresponding to amino acid residues 7-23 of the amino acid sequence of SEQ ID No. 4, has/have been deleted or replaced with one or more amino acid residues, which is/are present in an amino acid fragment corresponding to amino acid residues 13-45 of the amino acid
15 sequence shown in SEQ ID No. 10, or or in which one or more additional amino acid residues has/have been inserted using the relevant part of SEQ ID No. 10 or a corresponding part of another Fungamyl-like α -amylase as a template.

20 34. A variant of a parent Termamyl-like α -amylase, which variant has a region which, when the amino acid sequence of variant is aligned most closely with the amino acid sequence of the said parent α -amylase, occupies the same position as the portion from residue X to residue Y of SEQ ID No 4, the said
25 region having at least 80%, such as at least 90% sequence homology with the part of SEQ ID No 10 extending from residue Z to residue V of SEQ ID No 10, wherein
X is the amino acid occupying position 7 or 8 of SEQ ID No. 4,

30 Y is the amino acid occupying position 18, 19, 20, 21, 22 or 23 of SEQ ID No. 4,

Z is the amino acid occupying position 13 or 14 of SEQ ID No. 10, and

35

V is the amino acid occupying position 40, 41, 42, 43, 44 or 45 of SEQ ID No. 10.

35. The variant according to claim 33 or 34, in which the amino acid fragment of the parent α -amylase, which corresponds to amino acid residues 8-18 of SEQ ID No. 4, has been replaced with the amino acid fragment corresponding to amino acid residues 14-40 of the amino acid sequence shown in SEQ ID No. 10.

36. A variant of a parent Termamyl-like α -amylase, in which variant at least one of the amino acid residues of the parent α -amylase, which is present in a fragment corresponding to amino acid residues 322-346 of the amino acid sequence of SEQ ID No. 2, has/have been deleted or replaced with one or more amino acid residues, which is/are present in an amino acid fragment corresponding to amino acid residues 291-313 of the amino acid sequence shown in SEQ ID No. 10, or or in which one or more additional amino acid residues has/have been inserted using the relevant part of SEQ ID No. 10 or a corresponding part of another Fungamyl-like α -amylase as a template.

37. A variant of a parent Termamyl-like α -amylase, which variant has a region which, when the amino acid sequence of variant is aligned most closely with the amino acid sequence of the said parent α -amylase, occupies the same position as the portion from residue X to residue Y of SEQ ID No 2, the said region having at least 80% sequence homology with the part of SEQ ID No 10 extending from residue Z to residue V of SEQ ID No 10, wherein

X is the amino acid occupying position 322, 323, 324 or 325 of SEQ ID No. 2,

Y is the amino acid occupying position 343, 344, 345 or 346 of SEQ ID No. 2,

Z is the amino acid occupying position 291, 292, 293 or 294 of SEQ ID No. 10, and

V is the amino acid occupying position 310, 311, 312 or 313 of SEQ ID No. 10.

38. The variant according to claim 36 or 37, in which the amino acid fragment of the parent α -amylase, which corresponds to amino acid residues 325-345 of SEQ D No. 2, has been replaced with the amino acid fragment corresponding to amino acid residues 294-313 of the amino acid sequence shown in SEQ ID No. 10.

39. A variant of a parent Fungamyl-like α -amylase, in which variant at least one of the amino acid residues of the parent α -amylase, which is/are present in an amino acid fragment corresponding to amino acid residues 291-313 of the amino acid sequence of SEQ ID No. 10, has/have been deleted or replaced with one or more of the amino acid residues, which is/are present in an amino acid fragment corresponding to amino acid residues 98-210 of the amino acid sequence shown in SEQ ID No. 4, or in which one or more additional amino acid residues has/have been inserted using the relevant part of SEQ ID No. 4 or a corresponding part of another Termamyl-like α -amylase as a template.

20

40. A variant of a parent Fungamyl-like α -amylase, which variant has a region which, when the amino acid sequence of variant is aligned most closely with the amino acid sequence of the said parent α -amylase, occupies the same position as the portion from residue X to residue Y of SEQ ID No 10, the said region having at least 80%, such as at least 90% sequence homology with the part of SEQ ID No 10 extending from residue Z to residue V of SEQ ID No 4, wherein

X is the amino acid occupying position 117, 118, 119, 120 or 121 of SEQ ID No. 10,

Y is the amino acid occupying position 181, 182, 183, 184 or 185 of SEQ ID No. 10,

Z is the amino acid occupying position 98, 99, 100, 101 or 102 of SEQ ID No. 4, and

V is the amino acid occupying position 206, 207, 208, 209 or 210 of SEQ ID No. 4.

41. The variant according to claim 39 or 40, in which the amino acid fragment of the parent α -amylase, which corresponds to amino acid residues 121-181 of SEQ ID No. 10, has been replaced with the amino acid fragment corresponding to amino acid residues 102-206 of the amino acid sequence shown in SEQ ID No. 4.

10

42. A variant according to any of claims 39-41, in which the amino acid fragment of the parent α -amylase, which corresponds to amino acid residues 121-174 of SEQ ID No. 10, has been replaced with the amino acid fragment corresponding to amino acid residues 102-199 of the amino acid sequence shown in SEQ ID No. 4.

43. A variant of a parent Fungamyl-like α -amylase, in which an amino acid fragment corresponding to amino acid residues 181-184 of the amino acid sequence shown in SEQ ID No. 10 has been deleted.

45. A variant of a parent Termamyl-like α -amylase, which exhibits α -amylase activity and which has a decreased Ca^{2+} dependency as compared to the parent α -amylase.

46. A variant according to claim 45, which comprises a mutation in a position corresponding to at least one of the following positions in SEQ ID NO 2:

30 N104, A349, I479, L346, I430, N457, K385, F350, I411, H408 or G303, in particular a mutation corresponding to

N104D;

A349C+I479C;

L346C+I430C;

35 N457D,E;

N457D,E+K385R;

F350D,E+I430R,K;

F350D,E+I411R,K;

H408Q,E,N,D; and/or
G303N,D,Q,E.

47. A variant of a parent Termamyl-like α -amylase which
5 exhibits a higher activity below the pH optimum than the parent
 α -amylase, which variant comprises a mutation of an amino acid
residue corresponding to at least one of the following
positions of the *B. licheniformis* α -amylase (SEQ ID NO 2):
E336, Q333, P331, I236, V102, A232, I103, L196, in particular
10 at least one of the following mutations:

E336R,K;
Q333R,K; P331R,K;
V102R,K,A,T,S,G;
I236K,R,N;
15 I103K,R;
L196K,R; and/or
A232T,S,G.

48. A variant of a parent Termamyl-like α -amylase which
20 exhibits a higher activity above the pH optimum than the parent
 α -amylase, which variant comprises a mutation of an amino acid
residue corresponding to at least one of the following
positions of the *B. licheniformis* α -amylase (SEQ ID NO 2):
N236, H281 and/or Y273, in particular one of the following
25 mutations:

N326I,Y,F,L,V;
H281F,I,L; and/or
Y273F,W.

30 49. A variant of a parent Termamyl-like α -amylase which
exhibits α -amylase activity and which has an increased
thermostability and/or altered temperature optimum as compared
to the parent α -amylase, which variant comprises a mutation of
an amino acid residue corresponding to at least one of the
35 following positions of the *B. licheniformis* α -amylase (SEQ ID
NO 2):

L61, Y62, F67, K106, G145, I212, S151, R214, Y150, F143, R146, L241, I236, L7, V259, F284, F350, F343, L427 and/or V481, in particular at least one of the following mutations:

L61W,V,F;

5 Y62W;

F67W;

K106R,F,W;

G145F,W

I212F,L,W,Y,R,K;

10 S151 replaced with any other amino acid residue and in particular with F,W,I or L;

R214W;

Y150R,K;

F143W;

15 R146W;

L241I,F,Y,W;

I236L,F,W,Y;

L7F,I,W;

V259F,I,L;

20 F284W;

F350W;

F343W;

L427F,L,W; and/or

V481,F,I,L,W.

25

50. A variant of a parent Termamyl-like α -amylase, which exhibits α -amylase activity and which has a reduced capability of cleaving an oligo-saccharide substrate close to the branching point as compared to the parent α -amylase, which
30 variant comprises a mutation of an amino acid residue corresponding to at least one of the following positions of the *B. licheniformis* α -amylase (SEQ ID NO 2):

V54, D53, Y56, Q333 and/or G57, in particular at least one of
35 the following mutations:

V54L,I,F,Y,W,R,K,H,E,Q;

D53L,I,F,Y,W;

Y,56W;

Q333W; and/or

G57 to all possible amino acid residues.

51. The variant according to any of claims 17-50, wherein one
5 or more proline residues present in the amino acid residues
with which the parent α -amylase is modified are replaced with
a non-proline residue such as alanine.

52. The variant according to any of claims 17-51, wherein one
10 or more cysteine residues present in the amino acid residues
with which the parent α -amylase is modified are replaced with
a non-cysteine residue such as alanine.

53. A DNA construct comprising a DNA sequence encoding an α -
15 amylase variant according to any of claims 17-52.

54. A recombinant expression vector which carries a DNA con-
struct according to Claim 53.

20 55. A cell which is transformed with a DNA construct according
to Claim 53 or a vector according to Claim 54.

56. A cell according to Claim 55, which is a microorganism.

25 57. A cell according to Claim 56, which is a bacterium or a
fungus.

58. The cell according to Claim 57, which is a grampositive
bacterium such as *Bacillus subtilis*, *Bacillus licheniformis*,
30 *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*,
Bacillus alkalophilus, *Bacillus amyloliquefaciens*, *Bacillus*
coagulans, *Bacillus circulans*, *Bacillus lautus* or *Bacillus thu-*
ringiensis.

35 59. Use of an α -amylase variant according to any of claims 17-
52 for washing and/or dishwashing.

60. Use of an α -amylase variant according to any of claims 17-52 for desizing.
61. Use of an α -amylase variant according to any of claims 17-52 for starch liquefaction.
62. A detergent additive comprising an α -amylase variant according to any of claims 17-52, optionally in the form of a non-dusting granulate, stabilised liquid or protected enzyme.
63. A detergent additive according to Claim 62 which contains 0.02-200 mg of enzyme protein/g of the additive.
64. A detergent additive according to Claim 62 or 63, which additionally comprises another enzyme such as a protease, a lipase, a peroxidase, another amylolytic enzyme and/or a cellulase.
65. A detergent composition comprising an α -amylase variant according to any of claims 17-52.
66. A detergent composition according to Claim 65 which additionally comprises another enzyme such as a protease, a lipase, a peroxidase, another amylolytic enzyme and/or a cellulase.
67. A manual or automatic dishwashing detergent composition comprising an α -amylase variant according to any of claims 17-52.
68. A dishwashing detergent composition according to Claim 67 which additionally comprises another enzyme such as a protease, a lipase, a peroxidase, another amylolytic enzyme and/or a cellulase.
69. A manual or automatic laundry washing composition comprising an α -amylase variant according to any of claims 17-52.

70. A laundry washing composition according to Claim 69, which additionally comprises another enzyme such as a protease, a lipase, a peroxidase, an amylolytic enzyme and/or a cellulase.

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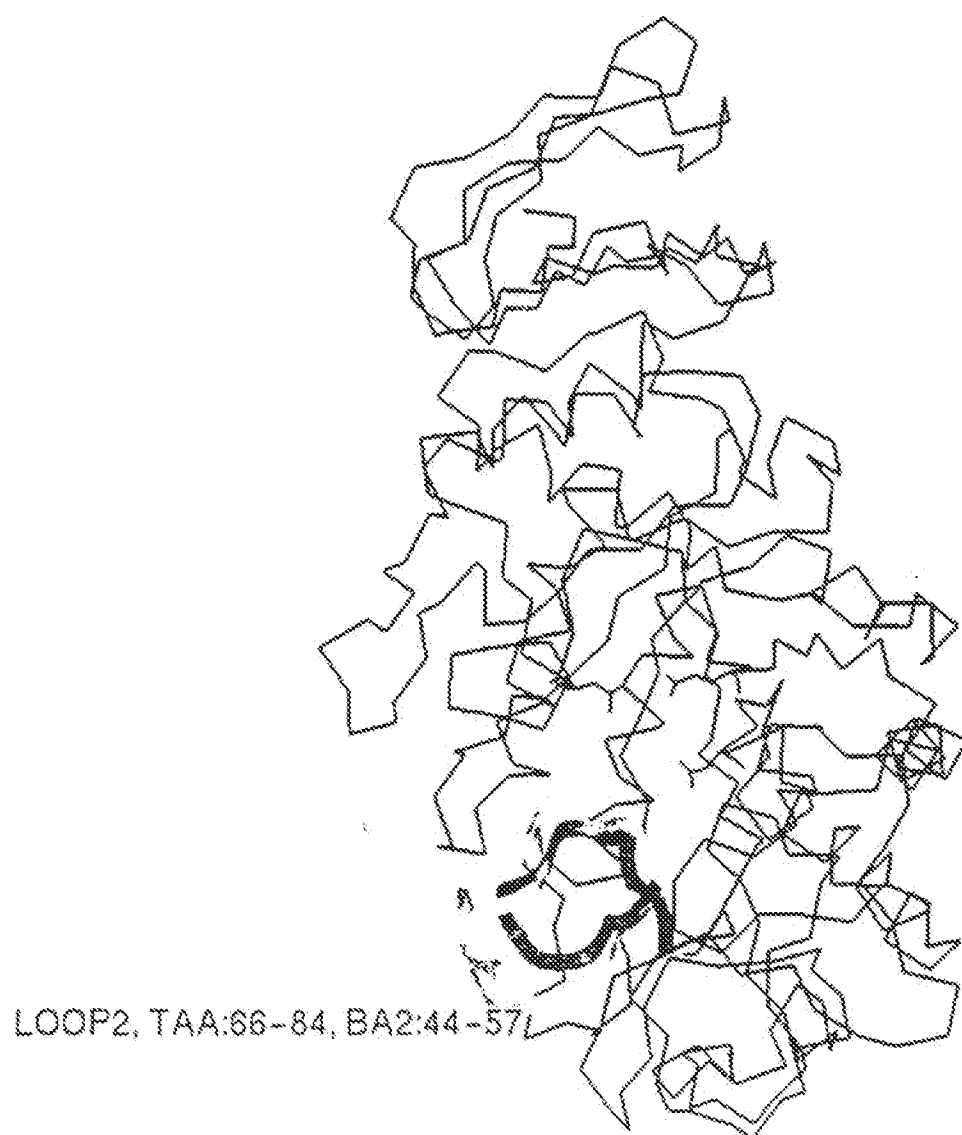


Fig. 1

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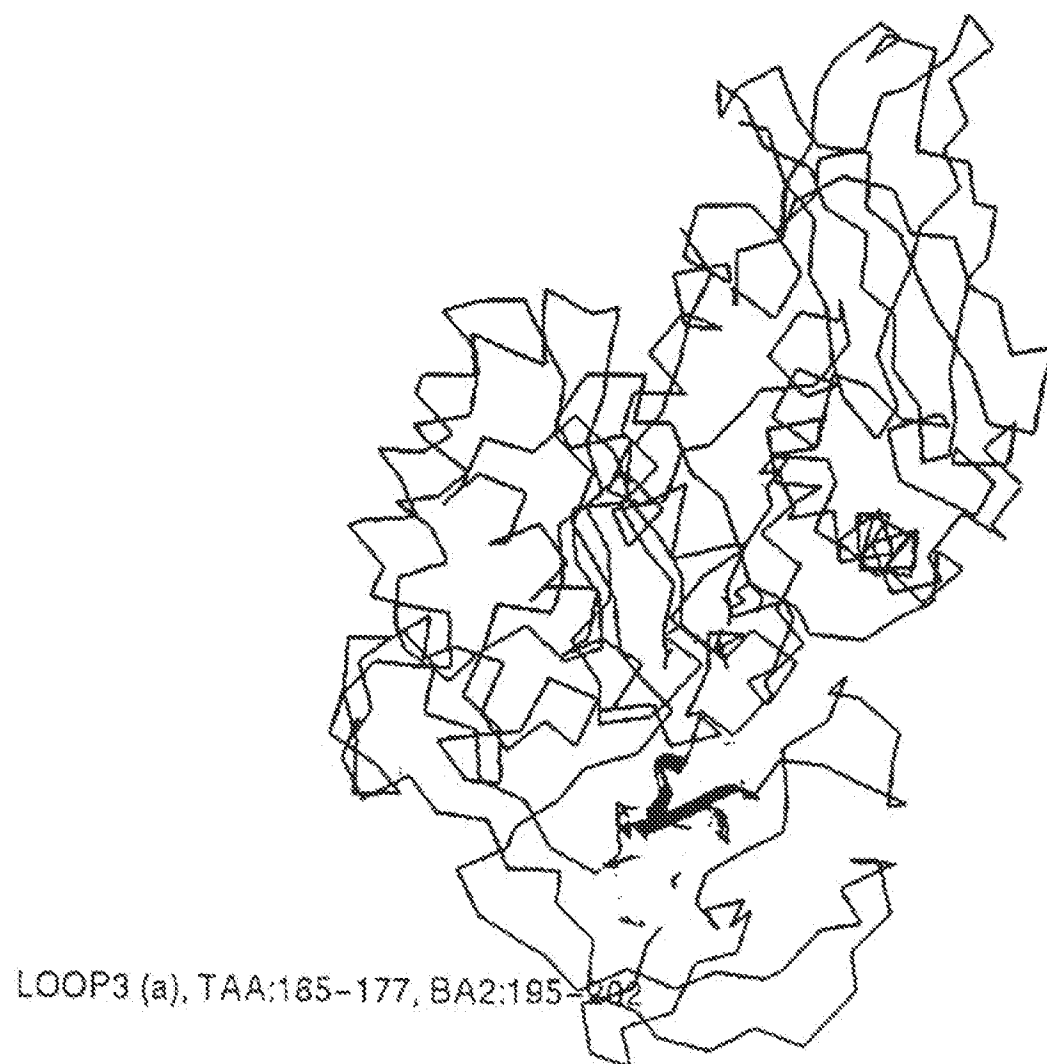


Fig. 2

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Fig. 3

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Fig. 4

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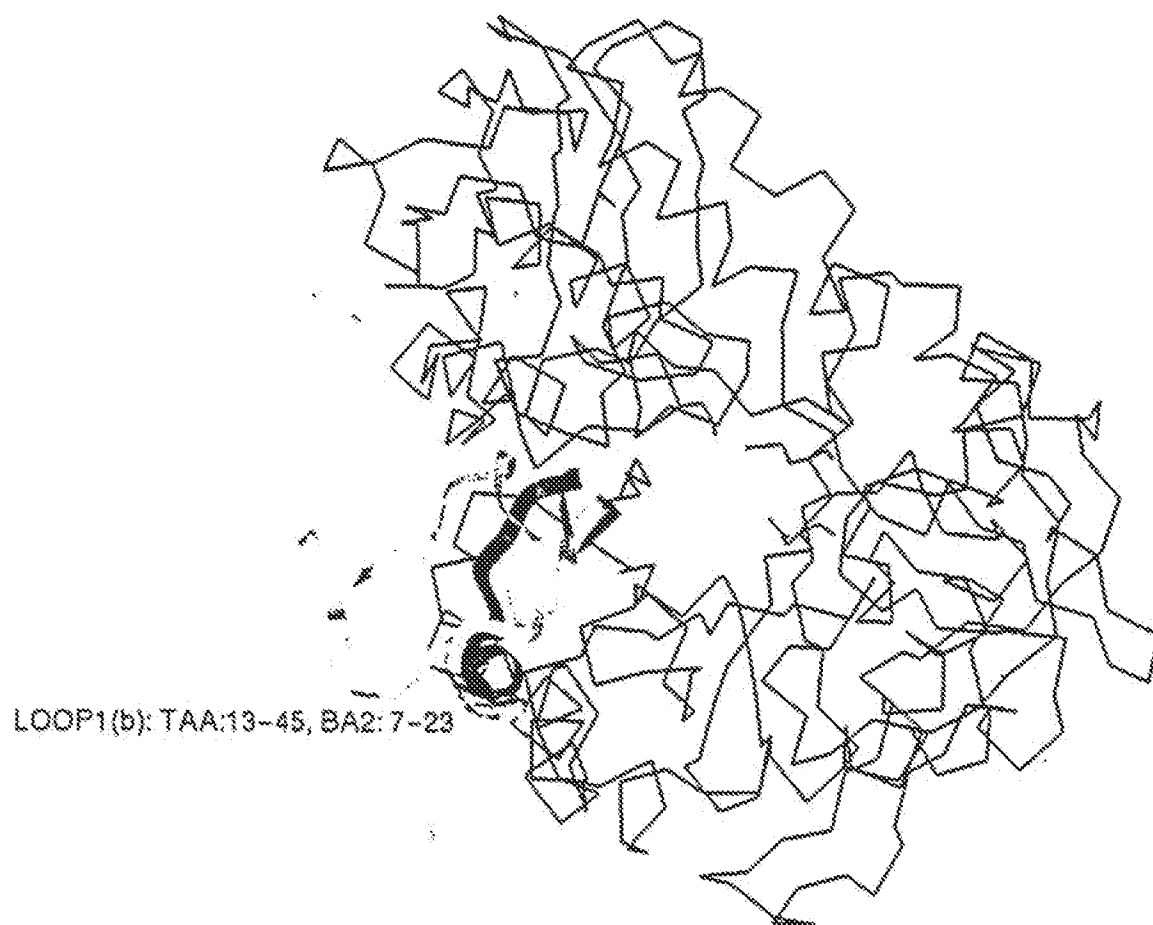


Fig. 5

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LOOP8:TAA:291-313, BA2: 322-346



Fig. 6

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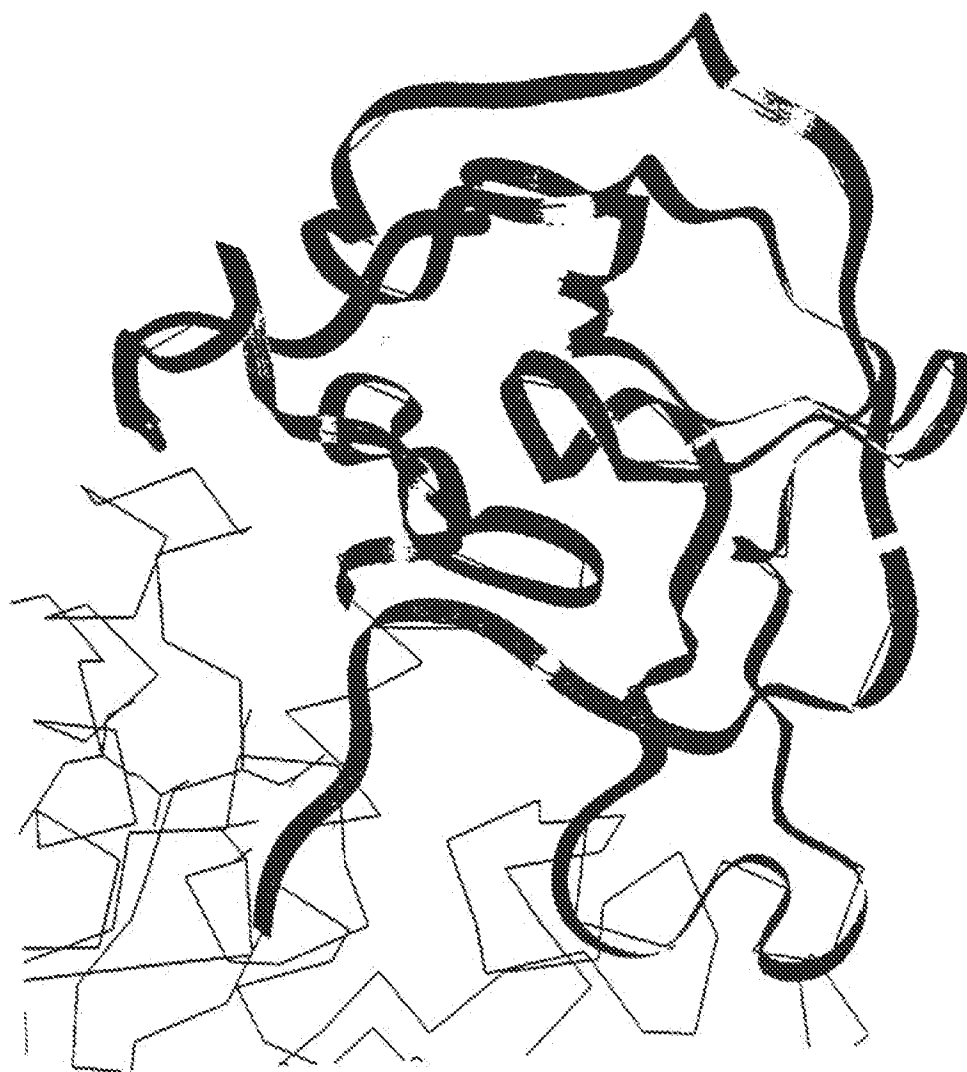


Fig. 7

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1
 CAT CAT AAT GGA ACA AAT GGT ACT ATG ATG CAA TAT TTC GAA TGG TAT TTG CCA AAT GAC
 H H N G T N G T M M Q Y F E W Y L F N D

21
 GGG AAT CAT TGG AAC AGG TTG AGG GAT GAC GCA OCT AAC TTA AAG AGT AAA GGG ATA ACA
 G N H W N R L R D D A A N L E S K G I T

41
 GCT GTA TGG ATC CCA CCT GCA TGG AAG GGG ACT TCC CAG AAT GAT GTA OCT TAT GGA GCC
 A V W I F P A W K G T S Q N D V G Y G A

61
 TAT GAT TTA TAT GAT CTT GGA GAG TTT AAC CAG AAG GGG ACG GTT CCG ACA AAA TAT GGA
 Y D L Y D L G E F N Q R G T V R T K Y G

81
 ACA CGC AAC CAG CTA CAG GCT GCG GTG ACC TCT TTA AAA AAT AAC GGC ATT CAG GTA TAT
 T R N Q L Q A A V T S L K N N G I Q V Y

101
 GGT GAT GTC GTC ATG AAT CAT AAA GGT GGA GCA GAT GGT ACG GAA ATT GTA AAT GCG GTA
 G D V V M N N K G G A D G T E I V N A V

121
 GAA GTG AAT CCG AGC AAC CCA AAC CAG GAA ACC TCA GGA GAG TAT GCA ATA GAA CCG TGG
 E V N R S N R N Q E T S G E Y A I E A W

141
 ACA AAG TTT GAT TTT CCT GGA AGA GGA AAT AAC CAT TCC AGC TTT AAG TGG CCG TGG TAT
 T K F D F F G R G N N H S S F X W R W Y

161
 CAT TTT GAT GGG ACA GAT TGG GAT CAG TCA CGC CAG CTT CAA AAC AAA ATA TAT AAA TTC
 R F D G T D W D Q S R Q L Q N K I Y K F

181
 AGG GGA ACA GGC AAG GCC TGG GAC TGG GAA GTC GAT ACA GAG AAT GGC AAC TAT GAC TAT
 R G T G E A W D W E V D T E N G N Y D Y

201
 CTT ATG TAT GCA GAC GTG GAT ATG GAT CAC CCA GAA GTA ATA CAT GAA CTT ACA AAC TGG
 L M Y A D V D M D H P E V I H E L R N W

221
 GGA GTG TGG TAT ACG AAT ACA CTG AAC CTT GAT GGA TTT AGA ATA GAT GCA GTG AAA CAT
 G V W Y T N T L N L D G P R I D A V K H

241
 ATA AAA TAT ACG TTT ACG AGA GAT TGG CTT ACA CAT GTG CGT AAC ACC ACA GGT AAA CCA
 I K V S F T R D W L T H V R N T T G K P

261
 ATG TTT GCA GTG GCT GAG TTT TGG AAA AAT GAC CTT GGT GCA ATT GAA AAC TAT TTT AAT
 H P A V A E F W K N D L G A I E N Y L N

281
 AAA ACA AGT TGG AAT CAC TGG GTG TTT GAT GTT CTT CTC CAC TAT AAT TTT TAC AAT GGA
 K T S W N H S V P D V P L H Y S L Y D A

Fig. 8

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301

TCT AAT AGC GGT GGT TAT TAT GAT ATG ACA AAT ATT TTA AAT GGT TCT GTG GTG CAA AAA
S N S G G Y Y D M R N I L N G S V V Q K

321

CAT CCA ACA CAT GCC GTT ACT TTT GTT GAT AAC CAT GAT TCT CAG CCC GGG CAA CCA TTG
H P T H A V T P V D N H D S Q P G E A L

341

GAA TCC TTT GTT CAA CAA TGG TTT AAA CCA CTT GCA TAT GCA TTG GTT CTG ACA AGG GAA
E S F V Q Q W F K P L A V A L V L T R E

361

CAA GGT TAT CCT TCC GTA TTT TAT GGG GAT TAC TAC GGT ATC CCA ACC CAT GGT GTT CCG
Q G Y P S V F Y G D Y Y G I P T R G V P

381

GCT ATG AAA TCT AAA ATA GAC CTT CTT CTG CAG GCA COT CAA ACT TTT GCC TAT GGT ACG
A N K S K I D P L L Q A R Q T F A Y G T

401

CAG CAT GAT TAC TTT GAT CAT CAT GAT ATT ATC GGT TGG ACA AGA GAG GGA AAT AGC TCC
Q H D Y P D H H D I I G W T R E G N S S

421

CAT CCA AAT TCA GGC CTT GCC ACC ATT ATG TCA GAT GGT CCA GGT GGT AAC AAA TGG ATG
H P N S G L A T I M S D G P G G N K W M

441

TAT GTG GGG AAA AAT AAA GCG GCA CAA GTT TGG AGA GAT ATT ACC GGA AAT AGG ACA GGC
Y V G X N K A G Q V W R D I T G N R T G

261

ACC CTC ACA ATT AAT GCA GAC GGA TGG GGT AAT TTC TCT GTT AAT GGA GGG TCC GTT TCG
T V T I N A D G W G N F S V N G G S V S

481

GTT TGG GTG AAG CAA TAA
V W V X Q *

Fig. 8 (cont.)

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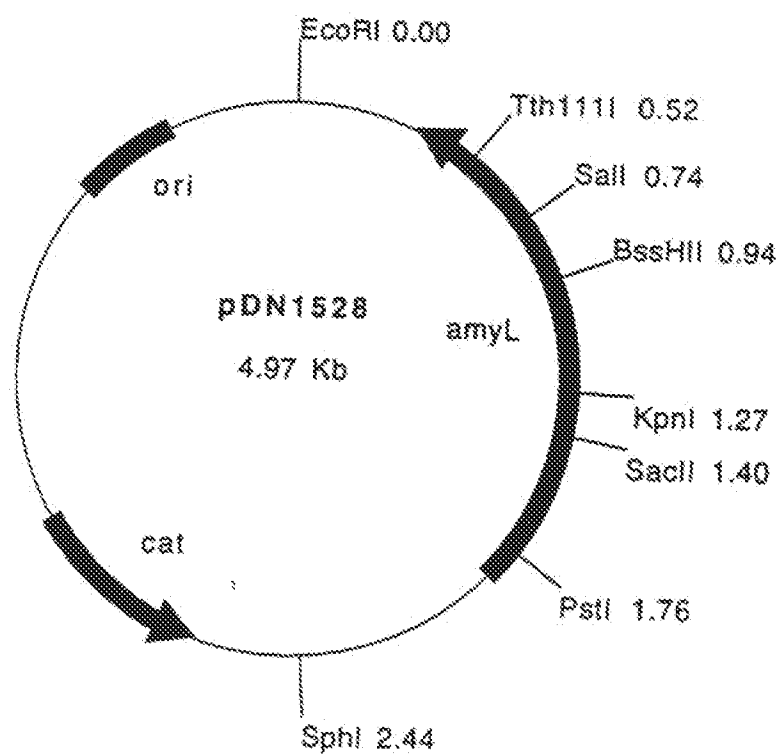


Fig. 9

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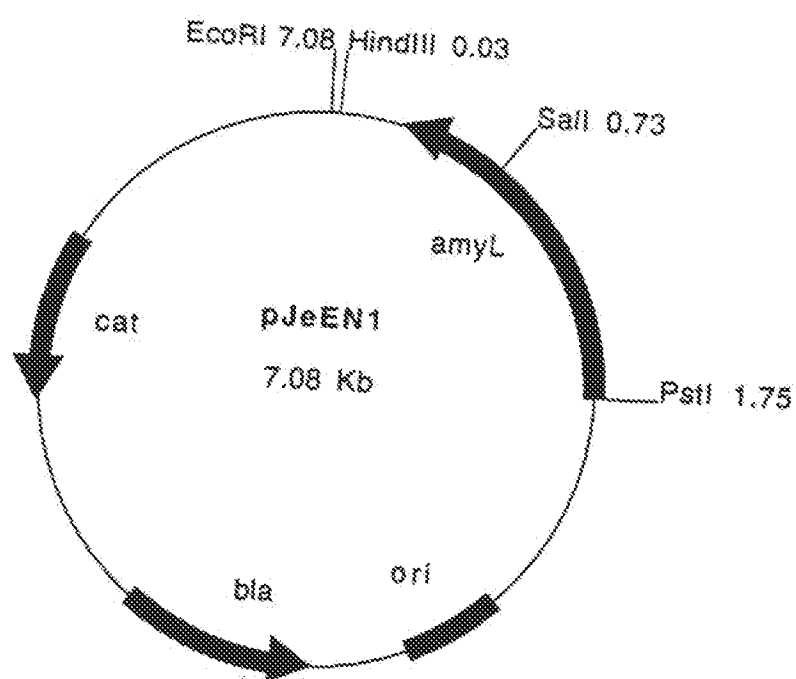


Fig. 10

INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK 96/00057

A. CLASSIFICATION OF SUBJECT MATTER

IPC6: C12N 9/28, C12N 15/56

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC6: C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

SE,DK,FI,NO classes as above

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

WPI, CA, MEDLINE, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	Dialog Information Services, File 5, BIOSIS PREVIEWS, Dialog accession no. 11619266, BIOSIS no. 98219266, Machius M et al: "Crystal structure of calcium-depleted Bacillus licheni- formis alpha-amylase at 2.2 A resolution", & Journal of Molecular Biology 246 (4). 1995. 545-559	1-17
X	Dialog Information Services, file 155, MEDLINE, Dialog accession no. 08974640, MEDLINE accession no. 94289640, Svensson B: "Protein engineering in the alpha-amylase family: catalytic mechanism, substrate specificity, and stability", & Plant Mol Biol (NETHERLANDS) May 1994, 25 (2) p141-57	1-17

☒ Further documents are listed in the continuation of Box C.
 ☒ See patent family annex.

* Special categories of cited documents.	"I" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A" document defining the general state of the art which is not considered to be of particular relevance	"X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E" earlier document but published on or after the international filing date	"Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&" document member of the same patent family
"O" document referring to an oral disclosure, use, exhibition or other means	
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

Date of mailing of the international search report

5 July 1996

05 -07- 1996

Name and mailing address of the ISA:

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The invention claimed relates to a method of constructing alpha-amylase variants with predetermined properties by comparing the three-dimensional structures of enzymes. The claims also include many alpha-amylase variants.

"A search for a special technical feature" as mentioned in PCT Rule 13.2 among the independent claims did not reveal a unifying, novel technical feature.

Accordingly, the following inventions were found:

- I Claims 1-17 focus on a method of constructing alpha-amylase variants by comparing the three-dimensional structure of a parent enzyme (Ternary-like alpha-amylase) with another enzyme e.g. mammalian or fungal alpha-amylases. The differences in structure are compared with the differences in function, whereafter new variants with new predictable characteristics are produced.
- II Claims 45-46 directed to a alpha-amylase variant that has decreased Ca^{2+} dependency,
- III Claim 47 directed to a alpha-amylase variant that exhibits higher activity below the pH-optimum than the parent enzyme.
- IV Claim 48 directed to a alpha-amylase variant having an increased thermostability and/or altered temperature optimum.
- V Claim 50 directed to a variant having reduced capability of cleaving an oligo-saccharide substrate close to its branching point.

Due to the complex construction of the claims and the fact that the search so far has not covered all aspects of the invention, it may be that further non-unity remarks can appear. If further searches are done, references might appear which will give further a posteriori non-unity remarks.

Therefore, the search has been restricted to the first invention.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK 95/00057

Claims 18-43 are directed to a number of different variants that are composed of several inventions. They are, however, so complex and broad that no meaningful search can be done, especially as no special characteristic is linked to the groups of variants. It is for example unlikely that claim 18 concerns one invention. It is not believable that a change in any amino acid in one fragment for one/or none of the amino acids in a fragment of another enzyme gives an enzyme with the same new and valuable characteristic. The formulation of claims 18-43 is so complicated because of all the different combinations of amino acid substitutions.

Thus they do not comply with Art. 6. PCT prescribing that claims shall be clear and concise.

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/DK 96/00057

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Dialog Information Services, file 155, MEDLINE. Dialog accession no. 08958150, MEDLINE accession no. 94273150, Nakatani H et al: "Effect of modifying histidine residues on the action of Bacillus amylo- liquefaciens and barley-malt alpha-amylases", & Carbohydr Res (NETHERLANDS) Apr 16 1994, 257 (1) p 155-61	1-17
Y	---	45-46
X	J. MED. BIOL., Volume 229, 1993, C. Chang et al, "Crystallization and Preliminary X-ray Crystallographic Analysis of alpha-Amylase from Bacillus subtilis" page 235 - page 238	1-17
A	WO 9100343 A2 (GIST-BROCADES N.V.), 10 January 1991 (10.01.91)	1-17
A	EP 0410498 A2 (GIST-BROCADES N.V.), 30 January 1991 (30.01.91)	1-17
A	JOURNAL OF BACTERIOLOGY, Volume 166, No 2, May 1986, G. L. Gray et al, "Structural Genes Encoding the Thermophilic alpha-Amylases of Bacillus stearothermophilus and Bacillus licheniformis" page 635 - page 643	1-17
P,X	WO 9535382 A2 (GISTBROCADES B.V.), 28 December 1995 (28.12.95), claims 1-2, abstract	45-46
Y	WO 9418314 A1 (GENENCOR INTERNATIONAL), 18 August 1994 (18.08.94)	45-46

INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK 96/00057

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Chemical Abstracts, Volume 108, No 11, 14 March 1988 (14.03.88), (Columbus, Ohio, USA), Buisson, G. et al, "Three dimensional structure of porcine pancreatic alpha-amylase at 2.9 Å resolution. Role of calcium in structure and activity", page 325, THE ABSTRACT No 90927h, EMBO J. 1987, 6 (13), 3909-3916 ---	45-46
Y	Chemical Abstracts, Volume 112, No 15, 9 April 1990 (09.04.90), (Columbus, Ohio, USA), Vihinen, Mauno et al, "Site-directed mutagenesis of a thermostable alpha-amylase from Bacillus stearothermophilus: putative role of three conserved residues", page 347, THE ABSTRACT No 135178r, J. Biochem 1990, 107 (2), 267-272 ---	45-46
A	US 4600693 A (KAREN L. KINDLE ET AL), 15 July 1986 (15.07.86) ---	45-46
A	Chemical Abstracts, Volume 112, No 19, 7 May 1990 (07.05.90), (Columbus, Ohio, USA), Holm, Liisa et al, "Random mutagenesis used to probe the structure and function of Bacillus stearothermophilus alpha-amylase", page 351, THE ABSTRACT No 174785f, Protein Eng. 1990, 3 (3), 181-191 -----	45-46

INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK96/00057

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

see next sheet
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see next sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
Claims 1-17 directed to a method of constructing alpha-amylase variants
and claims 45-46 directed to an alpha-amylase.
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☒ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No.

01/04/96

PCT/DK 96/00057

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO-A2- 9100343	10/01/91	AU-B, B- 629959 AU-A- 5939790 CA-A- 2032518 EP-A, A, A 0409299 JP-T- 4500609	15/10/92 17/01/91 30/12/90 23/01/91 06/02/92
EP-A2- 0410498	30/01/91	AU-B- 638263 AU-A- 5953890 CA-A- 2030554 CN-A- 1050220 JP-T- 4500756 US-A- 5364782 WO-A, A, A 9100353	24/06/93 17/01/91 30/12/90 27/03/91 13/02/92 15/11/94 10/01/91
WO-A2- 9535382	28/12/95	NONE	
WO-A1- 9418314	18/08/94	NONE	
US-A- 4600693	15/07/86	NONE	